

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 08:11:25 ; Search time 55 Seconds
(without alignments)
4126.196 Million cell updates/sec

Title: US-09-728-721-48

Perfect score: 740
Sequence: 1 cgcgtccgagcgcagcggggg.....atacgaagaacagctttaa 740

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCDS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	49.8	6.7	33529	US-09-144-085-3	Sequence 3, Appl
2	49.2	6.6	50937	US-09-428-517-1	Sequence 1, Appl
3	48	6.5	30001	US-08-125-468-1	Sequence 1, Appl
4	48	6.5	30001	US-08-474-933-1	Sequence 1, Appl
5	46.6	6.3	800	PCR-US95-04801-4	Sequence 4, Appl
6	46.2	6.2	23673	US-09-773-816-1	Sequence 1, Appl
7	44.6	6.0	1656	US-09-385-028-14	Sequence 14, Appl
8	44.6	6.0	15079	US-08-911-853-6	Sequence 6, Appl
9	44.4	6.0	1512	US-08-911-853-6	Sequence 6, Appl
10	44.4	6.0	1512	US-09-479-409-6	Sequence 6, Appl
11	44.4	6.0	1512	US-09-479-453-6	Sequence 6, Appl
12	44.4	6.0	17612	US-08-911-853-29	Sequence 29, Appl
13	44.4	6.0	17612	US-09-479-409-29	Sequence 29, Appl
14	44.4	6.0	17612	US-09-479-453-29	Sequence 29, Appl
15	44	5.9	4524	US-08-845-998-7	Sequence 7, Appl
16	44	5.9	4524	US-09-206-537-7	Sequence 7, Appl
17	44	5.9	4524	US-09-430-854-7	Sequence 7, Appl
18	43.8	5.9	861	US-08-997-080-97	Sequence 97, Appl
19	43.8	5.9	861	US-08-997-362-97	Sequence 97, Appl
20	43.8	5.9	861	US-08-873-970-97	Sequence 97, Appl
21	43.8	5.9	861	US-09-095-855-97	Sequence 97, Appl
22	43.8	5.9	861	US-09-324-542-97	Sequence 97, Appl
23	43.8	5.9	861	US-09-205-426-97	Sequence 97, Appl
24	43.8	5.9	1035	US-07-601-094-30	Sequence 30, Appl
25	43.8	5.9	1035	US-08-012-735-30	Sequence 30, Appl
26	43.8	5.9	1910	US-09-593-711A-3	Sequence 3, Appl
27	43.8	5.9	1914	US-07-601-094-1	Sequence 1, Appl

C	28	43.8	5.9	1914	1	US-08-012-735-1	Sequence 1, Appl
	29	43.6	5.9	43280	2	US-08-804-227C-1	Sequence 1, Appl
	30	43.6	5.9	44377	2	US-08-804-227C-7	Sequence 7, Appl
	31	43.6	5.9	44377	2	US-08-804-198-1	Sequence 1, Appl
	32	43.4	5.9	20235	3	US-07-642-734C-3	Sequence 3, Appl
	33	43.4	5.9	20235	3	US-08-439-009A-3	Sequence 3, Appl
	34	43.2	5.8	9551	1	US-08-056-200-93	Sequence 93, Appl
	35	43.2	5.8	9551	2	US-08-800-644-93	Sequence 93, Appl
	36	43	5.8	1209	4	US-09-105-537-21	Sequence 21, Appl
	37	43	5.8	1765	1	US-08-459-586-15	Sequence 15, Appl
	38	43	5.8	1765	2	US-08-282-696-15	Sequence 15, Appl
	39	43	5.8	13613	4	US-09-105-537-3	Sequence 3, Appl
	40	43	5.8	18994	1	US-08-459-586-4	Sequence 4, Appl
	41	43	5.8	18994	2	US-08-282-696-4	Sequence 4, Appl
	42	43	5.8	38506	3	US-09-320-878-19	Sequence 19, Appl
	43	42.6	5.8	1506	4	US-09-158-767-7	Sequence 7, Appl
	44	42.6	5.8	2261	4	US-09-158-767-1	Sequence 1, Appl
	45	42.2	5.7	1281	4	US-09-105-537-19	Sequence 19, Appl

ALIGNMENTS

```
RESULT 1
US-09-144-085-3
; Sequence 3, Application US/09144085
; Patent No. 6280999
; GENERAL INFORMATION:
; APPLICANT: Gustafsson, Claes
; APPLICANT: Betlach, Mary C.
; APPLICANT: Ashley, Gary
; APPLICANT: Jullien, Bryan
; APPLICANT: Ziemann, Rainer
; TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
; FILE REFERENCE: 30062-20020.20
; CURRENT APPLICATION NUMBER: US/09/144,085
; EARLIER FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: 09/010,809
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 33529
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-144-085-3

Query Match
Best Local Similarity 51.6%; Pred. No. 0.023;
Matches 114; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 90 GAGAACCTGACCGCCGAGGAGCTCAAGAGTTCAAGCTGAGCTGTCGTCGCTG 149
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 14083 GAGACGGTACGCGTGGCCGCGTGCGACGTGCAACGCGGAGAGGTCGCGTGG 14142
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 150 CCGGAGGCTACGCGGCATCCCGCGGCGCGCTCTGTGCATGACGCTTGAACCTC 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 14143 GCGCGCATGACGCGCGCGCGCGCTGACGCGCTGTGCACCTGCGCGCGCTCGAC 14202
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 210 ACCGACAGCTGCTGAGCTTCTACCTGAGACCTAGCGGCGGACGTCACCGCTAACGTC 269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 14203 GACGCGTGTCTCCCGCCAGACGCGCGACGCGCTTCTCGCGGTGCTGCGCGAAGCTG 14262
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 270 CTCGCGACATGGGCTCGCAGAGATGAGCGCCGACCTGCA 310
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 14263 GACGCGGCGCTGACCTGACGAGCTGACGCGGAGACTGGA 14303
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
US-09-428-517-1/C
; Sequence 1, Application US/09428517
; Patent No. 6251636
```

GENERAL INFORMATION:
APPLICANT: Bellach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 3062-20029.00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER FILING DATE: 1999-02-16
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1
LENGTH: 50937
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant DNA
US-09-428-517-1

Query Match 6.6%; Score 49.2; DB 4; Length 50937;
Best Local Similarity 47.7%; Pred. No. 0.034;
Matches 144; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 86 GCTGGAGAACCTGACCGCCGAGAGCTCAAGAGTTCAAGCTGAGCTGCTGTGGTCC 145
DB 1750 GCGGAGAGGCTGGCGGACCGCGCTGAGAGCTGATCCACTACCGGCTGGCGGAGG 1691
QY 146 GCTGGCGAGGGCTACGGGCGCATCCCGGGGCGCGCTGCTGTCTCATGAGCGCTTGA 205
DB 1690 CGGTGGAGGCGTACCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1631
QY 206 CCTGACCGACAGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 265
DB 1630 GCTGCGCGGAGGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1571
QY 266 GGTGCTGGCGGACATGGGCGCTGCGAGAGATGGCGGGAGAGTGGAGGCGCGCAC 325
DB 1570 GCGGATGATGAGGCGGTACGGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 1511
QY 326 GGGCTGTGAGCG 385
DB 1510 TCGGCG 1451

QY 386 CC 387
1450 CC 1449

RESULT 3
US-08-125-468-1/c
Sequence 1, Application US/08125468
Patent No. 5589385
GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy E.
APPLICANT: Pantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmids
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tseydos, Estelle J.
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-125-468-1

Query Match 6.5%; Score 48; DB 1; Length 30001;
Best Local Similarity 51.4%; Pred. No. 0.056;
Matches 111; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 140 GGTGCGGCTGCGGAGGCGCTACGGGCGCATCCCGGGGCGCGCTGTCTTCATGACGC 199
DB 29925 GATGCGGAACGCTGCGCAACTCGGCGAGCGCTGTGAGAGCTTCTTCTGCGTGG 29866
QY 200 CTGGACCTCACGACGAGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 259
DB 29865 CCTGCGCGTCCCGGT 29806
QY 260 CGCTAAGCTGTGCGCGCGCATGGGCGTGCAGAGATGGGCGGCGAGCTGCGAGGCG 319
DB 29805 CGCGCTGT 29746
QY 320 GCACGAGGCGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 355
DB 29745 GAGCGGCG 29710

RESULT 4
US-08-474-933-1/c
Sequence 1, Application US/08474933
Patent No. 5866410
GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy E.
APPLICANT: Pantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmids
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,933
FILING DATE:

Query Match	Score	46.2%	DB	4	Length	23673			
Best Local Similarity	46.4%	Pred.	No.	0.1					
Matches	150	Conservative	0	Mismatches	173	Indels	0	Gaps	0
QY	96	CTGACCGCCGAGAGACTCAGAGATTCAAGCTGAAGCTGCTGTGCGTGCCTGCGCGAG	155						
Db	10632	CTGACCGCCGCTGTATCAGACCGCTTCACGTCAGCGCAGCACTGTGCTGCGCGCGCAG	10691						

Oy	156	GGCTACGGGGCCATCCCGGGGGCGGGCTGTCCATGTAGACGCTTGAGACTCAACGAC	215
Db	10692	GACCCGCCGCCCGCATGAGGGCGGGCTACATTCGTGCAGTTCGTGTGGGAGACGACTGAA	10751
Oy	216	AAGCTGTGACCTTCTACCTGAGAGACCTACGAGCGCGAGCTACACGCTAAAGTCTGCG	275
Db	10752	GGGCTCGGGAATTTCTCCGAGCTGGCCACCGCTACAGATCTTATCATCGAGACTGGAAAGCC	10811
Oy	276	GACATGAGGCGCTCGAGAGATAGCGCGGGACGTGTGAGGGCGGCCACACGACAGAGGTCTGGA	335
Db	10812	CGCTGTCAATTCGAGGGGGGGGTATACGCACACACAGAGGGCGTGTGACTTACCCCCACCGCC	10871
Oy	336	GCCCGCCAGCTGGGATTCACAGGCGCCCTCTCTAAGTGTGGGACACCAACGACGCTGCATTT	395
Db	10872	TGAGCGCCCGCCACACACCGAGGAGGACACCCCTCATCGTATCGTGTGAAACACACCGTACCGT	10931
Oy	396	ATTAGACACGACCGGGGCTGCGCT	418
Db	10932	AGGGGCGCCGGCGGACTGTGGTCT	10954

RESULT 7

US-09-385-028-14/c
Sequence 14, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Kwamea A. Alido
APPLICANT: Ashish S. Paradar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biotynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
STREET: The Jenner Building, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P574520US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1656 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-385-028-14

Query Match	6.08;	Score 44.6;	DB 4;	Length 1656;
Best Local Similarity	47.68;	Pred. No. 0.17;		
Matches 13%, conservative	0;	Mismatches 144;	Indels 0;	Gaps 0;

OY	69	GACGGCATTCCGATCATCGCTGGAGAACTCACCGGCAGAGAGCTCAAGAATTCACGTG	128
Db	984	GTCTGATCCCTGGAGACCGTCAATGCCGACAAGTGTCGAAGAATCTAACCGGCTCAAGGAC	925
OY	129	AAGCTGCTGTGCGGTGCGCTGGCGAGAGGTATAGGGGACATCCCGCGGGGACGCTGTGTG	188
Db	924	ACCAGGGGCAAAAGCGGGTTGAAGACACCATGACCGCGGGGTCAAGTCCGCGCGCGGGCG	855
OY	189	TCCATAGAGACGCTTGGACACTCACCGAACAACCTGTCTACTCTTACCTCMGAGAGACCTAAGGC	248
Db	864	GCCCTGGAAGGCTCTGAAAGAAAGAACCGGGCATGTCTGCCGTCTACACCCCGCACCGGCAC	805
OY	249	GCCGAGCTACCGCTTAACGTGCTGTGCGGCAATGAGGCTCTGACAGAGATGATGCGCGGACGTG	308
Db	804	ATCTGTGGCGCGCGGAACCTGTGCTCCCTGGGATATAMCCCGGCGCTGAGAGGCGGCTACCG	745
OY	309	CAGGCGGCAACGCAACCAAGGCTCTGAGACCGGCGCC	343
Db	744	CCCGGCTTCAACTTCAAGGTGATGATACCACTGGCGGC	710

RESULT 8

US-09-385-028-1/C
Sequence 1, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Kwamea A. Aikoo
APPLICANT: Ashish S. Parashar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Blosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
STREET: The Jenifer Building, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent InRelease #1.0, Version #1.30 (Epo)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385, 028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Streptomyces clavuligerus
US-09-385-028-1

Query Match	6.0%;	Score 44.6;	DB 4;	Length 15079;
Best Local Similarity	47.6%;	Pred. No. 0.28;		
Matches 131; Conservative	0;	Mismatches 144;	Indels 0;	Gaps 0;

QY	69	GACCCATCTCTGGATGCGGCTGGAGAACCTGACCGCGAGACACTCAAGAATTCGAAGCTG	128
Db	1092	GTCTGTATCTTGGAACTGATGATGCCGCGACGGTGTGTAATAAATCTACCGGCTCAAGAAC	1033
QY	129	AAGTGTCTGTGCGGTGCGCTGTCCGCGAAGGGCTCAACGGGCGCATCCCGGGGCGCGCTGTG	188
Db	1032	ACGGAGGGCAAGCGGGGTGAAGACCACTATTCGACCCGGGCTCGACGCGCGCGCGGCG	973
QY	189	TCCATGAGAGCCCTTGGACCTCACCGACAGCTGTCAGCTTCTTACTGTGAACTACAGGC	248
Db	972	GCCCTGGAGGGCTTCGAAGAAGAACGGGGCGATGTGCGCTGTGACCCCGCACCGGGCAAC	913
QY	249	GCCGAGCTCACCCCTTAACCTGTGCGCCGATGTGGGCGTTCAGAGAATGAGCGCGGAGCTG	308
Db	912	ATCTGGCGCGCGGAAACGTGCCCTTCGGCGATGAACCGGGCGCTGGAAGGCGCGTACCGG	853
Y	309	CAGGCGGCCACGACCAAGGCGCTCTGGAGCGCGCGCC	343
Db	852	CCCGGCTCACCTTCAAGAGTGTACACCGGGGGC	818

RESULT 9
US-08-911-853-6

```

? Sequence 6, Application US/08911853
? Patent No. 6048710
?
? GENERAL INFORMATION:
? APPLICANT: Gerltse, Gjstbert
? APPLICANT: Quax, Wilhelmus J.
? TITLE OF INVENTION: EXPERIMENT SYSTEM FOR ALTERED
? TITLE OF INVENTION: EXPRESSION LEVELS
? NUMBER OF SEQUENCES: 37
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genencor International
? STREET: 925 Page Mill Road
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304-1013
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/911,853
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/699,092
? FILING DATE: 16-AUG-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Gaister, Debra J
? REGISTRATION NUMBER: 33,888
? REFERENCE/DOCKET NUMBER: GC361-2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-845-7620
? TELEFAX: 650-845-6504
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1512 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? OS-08-911-853-6

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Query Match	6.0%;	Score 44.4;	DB 3;	Length 1512;
Best Local Similarity	52.1%;	Pred. No. 0.1%;		
Matches 124;	Conservative 0;	Mismatches 111;	Indels 3;	Gaps 1;
53	CATGGGGGGGGGGGGGGCCCATCTTCGTGGAGAACTGACCGCCGAGAGCT	112		

Db	894	CTTGAAGCATGGCCAGACCCAGGTCAACCCGGGGGTGGCATGACCTTTGGCCCGCG	953
Qy	113	CAAGAAATTAAAGCTGAAGTGTCTGTGGGCGCGTGGCGAGGCTTACGGGGCGATCC	172
Db	954	CTTGGCGGCATCCTGGGCCAGGACCCGGACGTGTGATGTGTGGCGAGATCGCGACCA	1013
Qy	173	GGGGGGGGCGCTGTGTCATGTGAGCGCTTTGAGCTCACACGACAAAGTGGTACGGCTTCA	232
Db	1014	GGAGACCGCCGACATCGCCGTGACGGCGCTGG---CTCACCGGCGCAACCTGTGCTTCCAC	1070
Qy	233	CTGTGACACCTACGGGCGCAGGTCTTCAACCGCTAAACGTCGGCCGACATGGGCGTGCAG	290
Db	1071	CTGTGACACCAACAGCGCGCTGTGGCGCGCTCACACCGCGCTGTGTGACATGGCGTGTGAG	1128

RESULT 10
US-09-479-409-6

Sequence 6, Application US/09479409
Patent No. 6225106

GENERAL INFORMATION:
APPLICANT: Gerritse, Gijssbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genecore International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,409
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-479-409-6

Query Match	6.08;	Score 44.4;	DB 4;	Length 1512;
Best Local Similarity	52.18;	Pred. No. 0.19;		
Matches 124;	Conservative	0;	Mismatches	111;
			Gaps	3;

QY 53 CATGGGGGCGGGCGGGAGCCCATCTGGATGGCGTGGGAACCTGCAGCCGGCGAGAGACT 112
DB 894 CTTGGAGGACATGGCGCCAGACCCAGGTCAACCCGGGGGTGGCAATGACCTTGTGCCCGCGG 953
QY 113 CAGAAATTCAAGCTGAAGCTGCTGTGCGTGCCTGCCTGCAGGGGCTACGGGGCGCATCC 172
DB 954 CCTGCGGCGCATCTGGCGCCAGGACCCGGACAGTGGTGATGTCTGGCGAGATTCGGGAGCA 1013
QY 173 GCGGGGCGCGCTGCTGCATGGAGCCCTTGGACCTACCCGACAAAGTGGTACGCTTCA 232

ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,409
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-409-29

Query Match 6.0%; Score 44.4; DB 4; Length 17612;
Best Local Similarity 52.1%; Pred. No. 0.32; Mismatches 111; Indels 3; Gaps 1;
Matches 124; Conservative 0;
QY 53 CATGGGGCGCGCGCGAGCCATCTGGATGCTGGAGAGACTGACCGCGGAGAGCT 112
DB 11015 CCGTGAAGGATCGGCGAGACCCAGCCAGGTCACACCGGGGTGAGACCTTCGCCGCGG 11074
QY 113 CAGAGATTCAAGCTGAAGCTGCTGTGCTGCGCGCGAGGGCTACGCGGCGATCCC 172
DB 11075 CCGTGGCGCGATCTGCTGCGCGAGACCGAGACGCTGTGATGTGCGCGAGATCCGAGACCA 11134
QY 173 GCGGGGCGCGCTGTGCTGATGAGACCTTGAGCTCAACCGGACGATGAGCTTCA 232
DB 11135 GGAGACCGCGCGATCGCGCGTCAAGCCCTCG---CTCACCGCGCCACTGTGCTCTCCAC 11191
233 CCGTGAAGCTAAGCGCGCGAGCTCAGCGCTAACGCTGCTGCGCGAGATGCGGCTCGAG 290
DB 11192 CCGTGAACCAACAGCGCGCGTGGCGCGGTACCCGCGCTGCTGATGAGGCGGTGAG 11249

RESULT 14
US-09-479-453-29
Sequence 29, Application US/09479453
Patent No. 6313283
GENERAL INFORMATION:
APPLICANT: Gerritse, Gijbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-453-29

Query Match 6.0%; Score 44.4; DB 4; Length 17612;
Best Local Similarity 52.1%; Pred. No. 0.32; Mismatches 111; Indels 3; Gaps 1;
Matches 124; Conservative 0;
QY 53 CATGGGGCGCGCGCGAGCCATCTGGATGCTGGAGAGACTGACCGCGGAGAGCT 112
DB 11015 CCGTGAAGGATCGGCGAGACCCAGCCAGGTCACACCGGGGTGAGACCTTCGCCGCGG 11074
QY 113 CAGAGATTCAAGCTGAAGCTGCTGTGCTGCGCGAGGGCTACGCGGCGATCCC 172
DB 11075 CCGTGGCGCGATCTGCTGCGCGAGACCGAGACGCTGTGATGTGCGCGAGATCCGAGACCA 11134
QY 173 GCGGGGCGCGCTGTGCTGATGAGACCTTGAGCTCAACCGGACGATGAGCTTCA 232
DB 11135 GGAGACCGCGCGATCGCGCGTCAAGCCCTCG---CTCACCGCGCCACTGTGCTCTCCAC 11191
233 CCGTGAAGCTAAGCGCGCGAGCTCAGCGCTAACGCTGCTGCGCGAGATGCGGCTCGAG 290
DB 11192 CCGTGAACCAACAGCGCGCGTGGCGCGGTACCCGCGCTGCTGATGAGGCGGTGAG 11249

RESULT 15
US-08-845-998-7
Sequence 7, Application US/08845998
Patent No. 5879892
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coule, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 174..1433
US-08-845-998-7

```

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Query Match
Best Local Similarity 5.9%; Score 44; DB 2; Length 4524;
Matches 180; Conservative 0; Mismatches 175; Indels 11; Gaps 2;

OY 21 TGAGCGGCGGCGAGCCGCGGAGATCTGAGACCATGAGGCGCGCGGAGCGCATCTG 80
Db 556 TGGCCGCGCGCGGCGCGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 615
OY 81 GATGCGCTGAGAACCTGACCGCGGAGAGCTCAAGAGTTCAGAGTGAAGTCTGCTG 140
Db 616 GGGGCGGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 675
OY 141 GTGCCGCTG--CGGAGGGCTACGCGGCGCATCCGCGGCGCGCGCGCTGTTCATGAGC 198
Db 676 GCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 735
OY 199 CCTTGACCTACCGAAGCTGTGCTTACCTGAGAGCTACGCGCGCGAGCTCA 258
Db 736 GGCACCCCTACCGCATATGACAGGCTTGCGCACCTGTGCGACCCGCGCGCGCGCG 795
OY 259 CCGCTAACGCTGCTCGCGGACATGGGCTTGCAAGAGATGGCGGCGAGCTGCAAGCGGCA 318
Db 796 CCATGAACATGCTGCTCGGCGCTGCGCAC-----CCGGCTGTGTGGCGCGCG 846
OY 319 CGCACAGGCGCTGAGACCGCGCCAGCTGGGATCCAGGCCCTCTCTAGTGGGAGCA 378
Db 847 CGCACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 906
OY 379 AGCGAG 384
Db 907 CGGCGG 912

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Search completed: December 13, 2002, 08:28:31
Job time : 275 secs

us-09-728-721-48.rng

Page 2

[illegible]

CC Caspase-1, CARD-7 and itself. CARD-5 can, therefore, modulate CARD-5
CC activity and NF-kappaB activation, regulate cell growth and cell death
CC and be used in gene therapy. The CARD-5 polypeptides are useful for
CC identifying compounds which bind to them and modulate their activity for
CC detecting the presence of CARD-5 in a sample. CARD-5 polypeptides, and
CC nucleic acids, antibodies and modulators of CARD-5 expression or activity
CC can be used to treat immune disorders such as chronic inflammatory
CC diseases and disorders, Hashimoto's thyroiditis, graft inflammatory
CC sarcoidosis, atopic conditions (such as asthma and allergy), glomerular
CC nephritis, human immunodeficiency virus (HIV) and bacterial infections
CC (including tuberculosis and lepromatous leprosy) and in screening and
CC detection assays. Modulators of CARD-5 activity or expression are also
CC useful for treating autoimmune disorders, such as systemic lupus
CC erythematosus and arthritis, cell depletion, neurological disorders,
CC such as Alzheimer's disease, Parkinson's disease and spinal muscular
CC atrophy, hematologic diseases, such as myelodysplastic syndrome and
CC aplastic anemia, myocardial infarction and stroke. The sequence
CC presented is the complementary strand to the human caspase recruitment
CC domain-5 (CARD-5) cDNA.

Sequence 740 BP; 120 A; 236 C; 238 G; 146 T; 0 other;

Query Match 100.0%; Score 740; DB 24; Length 740;
Best Local Similarity 100.0%; Pred. No. 2e-147;

Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCGTCGGGTCGACGGGGTGAACGGCGGCGGCGGATCTCGAGCCATGAGGCG 60
DB 740 CGCGTCGGGTCGACGGGGTGAACGGCGGCGGCGGATCTCGAGCCATGAGGCG 60
OY 61 GCGCGCGGACGGCCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 681
DB 680 GCGCGCGGACGGCCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 681
OY 121 TCAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
DB 620 TCAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
OY 181 CGCTGCTGCATGAGACGCTTTGATCTCAACGAGTGTCAAGCTTTCACTGAGAGA 240
DB 560 CGCTGCTGCATGAGACGCTTTGATCTCAACGAGTGTCAAGCTTTCACTGAGAGA 240
OY 241 CCTACGGGCGGAGCTCAACGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
DB 500 CCTACGGGCGGAGCTCAACGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
OY 301 GGCAGCTGAGGCGGCGGACGACGAGGCTTGAAGCCGCGCCAGCTGGATCCAGGCC 441
DB 440 GGCAGCTGAGGCGGCGGACGACGAGGCTTGAAGCCGCGCCAGCTGGATCCAGGCC 360
OY 361 CTCTCAGTGGGCGGACGAGCTTGAATATGACACGACGAGGCTGGGCTTGA 420
DB 380 CTCTCAGTGGGCGGACGAGCTTGAATATGACACGAGGCTGGGCTTGA 420
OY 421 TCGGAGAGGTCAAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 321
DB 320 TCGGAGAGGTCAAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 480
OY 481 ATGAGAGTACACGAGGAGTGGGGCGGCGGCGGACCAACCAACGAGATGCGAGAGCT 261
DB 260 ATGAGAGTACACGAGGAGTGGGGCGGCGGCGGACCAACCAACGAGATGCGAGAGCT 540
OY 541 TCAGTTTACACGAGCTGAGAACTGAGAACTGAGAACTGAGAACTGAGAACTGAGAACT 201
DB 200 TCAGTTTACACGAGCTGAGAACTGAGAACTGAGAACTGAGAACTGAGAACTGAGAACT 600
OY 601 AGTCCAGTCTACTGCTGTGAGAGTCTGAGAGGAGTCTGAGAGGCTCTCCACCAACAC 141
DB 140 AGTCCAGTCTACTGCTGTGAGAGTCTGAGAGGAGTCTGAGAGGCTCTCCACCAACAC 660
OY 661 TCGGTCAGAGCCCTGGCAATCCCAACCAATCTGATCTGATCTTTTATACCAAT 81
DB 80 TCGGTCAGAGCCCTGGCAATCCCAACCAATCTGATCTGATCTTTTATACCAAT 720
121

OY 721 ATACGAAAGCCAGCTTGAA 740
DB 20 ATACGAAAGCCAGCTTGAA 1

RESULT 4

ID AAD03890 standard; cDNA; 770 BP.

AC AAD03890;

DT 02-JUL-2001 (first entry)

DE Human target of methylation-induced silencing-1 (TMS1) cDNA.

KW Human; target of methylation-induced silencing-1; TMS1; cytostatic;
KW antiproliferative; apoptosis inducer; gene therapy; CpG island;
KW caspase-recruiting domain; CARD; cancer; breast; ss.

OS Homo sapiens.

FT Key Location/Qualifiers
FT CDS 75..662 /tag="a /product="Human TMS1 protein"

WO200129235-A2.

26-APR-2001.

18-OCT-2000; 2000WO-US28747.

18-OCT-1999; 99US-0159975.

(UYEW-) UNIV EMORY.

Vertino PM;

WPI: 2001-290922/30.

P-PSDB; AAE00586.

PT Novel gene TMS1, transcriptionally silenced due to increased
PT methylation useful for identifying subject at risk of developing tumor
PT characterized by abnormal methylation, for treating cancer by inducing
PT apoptosis -

PS Claim 68; Page 113-114; 124pp; English.

CC The invention relates to identification of target of methylation-induced
CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to
CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1
CC consists of a carboxy terminal caspase-recruiting domain (CARD) and
CC plays a role in induction of apoptosis. TMS1 gene and protein are useful
CC as tools for diagnosis and treating a subject at risk of developing
CC cancer (e.g. breast cancer) characterized by abnormal CpG methylation or
CC abnormally low levels of TMS1 expression products. Unique fragments of
CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy.
CC Increasing TMS1 polypeptide level to an above normal level. The CpG
CC island region of TMS1 or its fragments are used to study the methylation
CC patterns apart from any coding region contained in it.
CC The present sequence is human target of methylation-induced silencing-1
CC (TMS1) cDNA.

SQ Sequence 770 BP; 157 A; 247 C; 241 G; 125 T; 0 other;

Query Match 99.2%; Score 734; DB 22; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.7e-146;

Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CGCGTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 66
|||||

Db 28 CGGCTGACAGGGGAGTGGAGGCGGACGGCCGGGAGTCTGGAGCCATGGGCGGCGG 87
QY 67 GCGAGCCCATCTCTGGATGGGCTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 126
Db 88 GCGAGCCCATCTCTGGATGGGCTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 147
QY 127 TGAAGCTGCTGTGGGCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 186
Db 148 TGAAGCTGCTGTGGGCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 207
QY 187 TGTTCATGGAGCGCTTGGACCTCACCAGCAAGCTGGTCACTTCTACCTGAGAACCTAG 246
Db 208 TGTTCATGGAGCGCTTGGACCTCACCAGCAAGCTGGTCACTTCTACCTGAGAACCTAG 267
QY 247 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCGAGAGATGGCGGCGAG 306
Db 268 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCGAGAGATGGCGGCGAG 327
QY 307 TGCAGGCGGCGACGACGAGGAGGCTGGAGCGGCGGAGCTGGAGTCCAGGCGGCTCC 366
b 328 TGCAGGCGGCGACGACGAGGAGGCTGGAGCGGCGGAGCTGGAGTCCAGGCGGCTCC 387
QY 367 AGTCGCGACGCAAGCGAGGCTGCACTTTATAGCCAGCAGCGGCTGGCTTATGCGA 426
Db 388 AGTCGCGACGCAAGCGAGGCTGCACTTTATAGCCAGCAGCGGCTGGCTTATGCGA 447
QY 427 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTACGCGGAAGTCTGACGATGAGC 486
Db 448 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTACGCGGAAGTCTGACGATGAGC 507
QY 487 AGTACCAGCAGTGGGCGGCGGAGCCACCAACCAAGAGGAGGAGGAGGAGGAGGAGG 546
Db 508 AGTACCAGCAGTGGGCGGCGGAGCCACCAACCAAGAGGAGGAGGAGGAGGAGGAGG 567
QY 547 TCACACGACGCTGGAAGCTGGAAGCTGGAAGGACTTGTCTCCAGGCGCTTAAGGAGTCC 606
Db 568 TCACACGACGCTGGAAGCTGGAAGGACTTGTCTCCAGGCGCTTAAGGAGTCC 627
QY 607 AGTCCACTGCTGGAGGAGCTGGAGCGGAGCTGAGGCTCTTCCAGCAACACTCCGGT 666
Db 628 AGTCCACTGCTGGAGGAGCTGGAGCGGAGCTGAGGCTCTTCCAGCAACACTCCGGT 687
QY 667 CAGCCCTGGCAATCCCAATCATCTGAAATGATCTTTTATACCAATATACGA 726
Db 688 CAGCCCTGGCAATCCCAATCATCTGAAATGATCTTTTATACCAATATACGA 747
QY 727 AAAGCCAGCTTGA 740
b 748 AAAGCCAGCTTGA 761
RESULT 5
ID AAL47126 standard; DNA; 782 BP.
AC AAL47126;
XX 20-AUG-2002 (first entry)
DE Pyrin domain containing protein Pycard coding sequence.
XX Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
KW antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
KW neuroprotective; antiarthritic; antirheumatic; antiasthmatic;
KW nephrotoxic; osteopathic; neurotoxic; intracellular signal transduction;
KW inflammation; Alzheimer's disease; infection; psoriasis; asthma;
KW arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
KW osteoarthritis; glomerulonephritis; gene; ds.
OS Unidentified.
XX
XX
XX WO200240668-A2.
XX
XX

PD 23-MAY-2002.
XX
XX 30-OCT-2001: 2001WO-EP12545.
XX
XX 15-NOV-2000: 2000DE-1056687.
PR 30-NOV-2000: 2000DE-1059595.
XX
XX (APOT-) APOTEC RES & DEV LTD.
PA
XX
PI Tschopp J, Martinon F;
PI
DR MPI: 2002-427093/45.
DR P-PSDB; AAO17854.
XX
XX New DNA encoding protein with pyrin domain, useful for treating
PT diseases involving impaired signal transduction, particularly
PT inflammation, also proteins and antibodies -
XX
XX
PS Claim 5; Fig 1; 116pp; German.
XX
XX The present invention relates the DNA and their encoded proteins, where
CC the proteins contain at least one PYD (pyrin) domain. These can be used
CC to treat diseases associated with impaired intracellular signal
CC transduction, particularly inflammation such as psoriasis,
CC arteriosclerosis, bacterial or viral infections (particularly meningitis
CC and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
CC sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
CC and Parkinson's diseases. The present sequence is a coding sequence of
XX the invention.
XX
SQ Sequence 782 BP; 158 A; 251 C; 246 G; 127 T; 0 other;
Query Match 99.2%; Score 734; DB 24; Length 782;
Best Local Similarity 100.0%; Pred. No. 3.7e-146;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCGCTGACAGGGGAGTGGAGGCGGCGGAGGAGGAGTCTGGAGGAGGAGGAGGAGG 66
Db 40 CCGCTGACAGGGGAGTGGAGGCGGCGGAGGAGGAGGAGTCTGGAGGAGGAGGAGGAGG 99
QY 67 GCGAGCCCATCTCTGGATGGGCTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 126
Db 100 GCGAGCCCATCTCTGGATGGGCTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 159
QY 127 TGAAGCTGCTGTGGGCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 186
Db 160 TGAAGCTGCTGTGGGCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 219
QY 187 TGTTCATGGAGCGCTTGGACCTCACCAGCAAGCTGGTCACTTCTACCTGAGAACCTAG 246
Db 220 TGTTCATGGAGCGCTTGGACCTCACCAGCAAGCTGGTCACTTCTACCTGAGAACCTAG 279
QY 247 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCGAGAGATGGCGGCGAGC 306
Db 280 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCGAGAGATGGCGGCGAGC 339
QY 307 TGCAGGCGGCGACGACGAGGAGGCTGGAGCGGCGGAGCTGGAGTCCAGGCGGCTCC 366
Db 340 TGCAGGCGGCGACGACGAGGAGGCTGGAGCGGCGGAGCTGGAGTCCAGGCGGCTCC 399
QY 367 AGTCGCGACGCAAGCGAGGCTGCACTTTATAGCCAGCAGCGGCTGGCTTATGCGA 426
Db 400 AGTCGCGACGCAAGCGAGGCTGCACTTTATAGCCAGCAGCGGCTGGCTTATGCGA 459
QY 427 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTACGCGGAAGTCTGACGATGAGC 486
Db 460 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTACGCGGAAGTCTGACGATGAGC 519
QY 487 AGTACCAGCAGTGGGCGGCGGAGCCACCAACCAAGAGGAGGAGGAGGAGGAGGAGG 546
Db 520 AGTACCAGCAGTGGGCGGCGGAGCCACCAACCAAGAGGAGGAGGAGGAGGAGGAGG 579
QY 547 TCACACGACGCTGGAAGCTGGAAGGACTTGTCTCCAGGCGCTTAAGGAGTCC 606

CC the present invention.

SQ * Sequence 811 BP; 170 A; 253 C; 259 G; 128 T; 1 other:

Query Match 94.3%; Score 697.6; DB 21; Length 811;
 Best Local Similarity 99.5%; Pred. No. 1.9e-138;
 Matches 730; Conservative 1; Mismatches 0; Indels 3; Gaps 3;

QY 7 CGGCTGCAGCGGGGTGACGGGGGCGAGGGGCGGGATCTTGAGACCATGGGGCGCGGC 66
 DB 68 CGGCTGCAGCGGGGTGACGGGGGCGAGGGGCGGGATCTTGAGACCATGGGGCGCGGC 127
 QY 67 GCGAGCCATCTTGATGCGCTGAGAACTGACCGCGAGAGGCTCAAGAGTTCAAGC 126
 DB 128 GCGAGCCATCTTGATGCGCTGAGAACTGACCGCGAGAGGCTCAAGAGTTCAAGC 187
 QY 127 TGAAGCTCTGTGGTGGCTGCGCGAGGGGCTACGGGGCGATCCGGGGGCGCGCTGC 186
 DB 188 TGAAGCTCTGTGGTGGCTGCGCGAGGGGCTACGGGGCGATCCGGGGGCGCGCTGC 247
 QY 187 TGTCCATGGAGCCCTTGAGACCTGACGACCAAGCTGTGACCTTCACTGAGACTACG 246
 DB 248 TGTCCATGGAGCCCTTGAGACCTGACGACCAAGCTGTGACCTTCACTGAGACTACG 307
 QY 247 GCGCCGAGCTCACCGCTAAAGTGTGCGGACATGGGCTGCGAGAGATGGCGGGGACG 306
 DB 308 GCGCCGAGCTCACCGCTAAAGTGTGCGGACATGGGCTGCGAGAGATGGCGGGGACG 367
 QY 307 TGCAGGCGGCGCAGCAGCAGGCGCTGTGAGCCGCGCAGCTGGATGCCAGGCCCTCTC 366
 DB 368 TGCAGGCGGCGCAGCAGCAGGCGCTGTGAGCCGCGCAGCTGGATGCCAGGCCCTCTC 427
 QY 367 AGTCGGGACCCCAAGCCAGGCGCTGTGATGATGACCAAGCAGCGGCGCTTATCGCA 426
 DB 428 AGTCGGGACCCCAAGCCAGGCGCTGTGATGATGACCAAGCAGCGGCGCTTATCGCA 487
 QY 427 GGGTACAAAGCTTGATGGTGTGCTGATGCTCTGTAGCGGAGAGGCTGAGAGTGAAC 486
 DB 488 GGGTACAAAGCTTGATGGTGTGCTGATGCTCTGTAGCGGAGAGGCTGAGAGTGAAC 547
 QY 487 AGTACCAAGCAGTGGGGGCGAGCCCAACCAAGCAAGATGGCGAGCTCTTCAATT 546
 DB 548 AGTACCAAGCAGTGGGGGCGAGCCCAACCAAGCAAGATGGCGAGCTCTTCAATT 606
 QY 547 TCACACCAAGCCTGAGACCTGAGACTGCAAGACTTCTCTCCAGGCGCTTAAGGAGTCCC 606
 DB 607 TCACACCAAGCCTGAGACCTGAGACTGCAAGACTTCTCTCCAGGCGCTTAAGGAGTCCC 666
 QY 607 AGTCTTACCTGGTGGAGGAGCTGAGAGGAGCTGAGGCTCTTCCAGCAACATCCGGT 666
 DB 667 AGTCTTACCTGGTGGAGGAGCTGAGAGGAGCTGAGGCTCTTCCAGCAACATCCGGT 725
 QY 667 CAGCCCTGGGCAATCCCAACCAATCATCTGATCTGATCTTTTATACAAATATACGA 726
 DB 726 CA-SCCTGGGCAATCCCAACCAATCATCTGATCTGATCTTTTATACAAATATACGA 784
 QY 727 AAAGCCAGCTTGA 740
 DB 785 AAAGCCAGCTTGA 798

RESULT 10

AAD03906 standard; cDNA: 713 BP.

AAD03906;

02-JUL-2001 (first entry)

Alternatively spliced form of human TMS1 cDNA (lacking exon2).

Human: target of methylation-induced silencing-1; TMS1; cytosstatic;
 antiapoptotic; apoptosis inducer; gene therapy; CpG island;

KW caspase-recruiting domain; CARD; cancer; breast; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 75..605
 FT /tag= a
 FT /product= "Alternatively spliced form of human TMS1
 protein lacking exon2"

PI W0200129235-A2.

PD 26-APR-2001.

PR 18-OCT-2000; 2000WO-US28747.

PX 18-OCT-1999; 99US-0159975.

PY (UYEM-) UNIV EMORY.

PI Vertino PM.

DR WPI; 2001-290922/30.

DR P-PSDB; AAE00594.

PT Novel gene TMS1, transcriptionally silenced due to increased
 PT methylation useful for identifying subject at risk of developing tumor
 PT characterized by abnormal methylation, for treating cancer by inducing
 PT apoptosis

PS Claim 68; Page 122; 124pp; English.

XX The invention relates to identification of target of methylation-induced
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and
 CC plays a role in induction of apoptosis. TMS1 gene and protein are useful
 CC as tools for diagnosing and treating a subject at risk of developing
 CC cancer (e.g. breast cancer) characterized by abnormal CpG methylation or
 CC abnormally low levels of TMS1 expression products. Unique fragments of
 CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy.
 CC TMS1 molecule is also useful for treating abnormal cell proliferation by
 CC increasing TMS1 polypeptide level to an above normal level. The CpG
 CC island region of TMS1 or its fragments are used to study the methylation
 CC patterns apart from any coding region contained in it.
 CC The present sequence is alternatively spliced form of human target of
 CC methylation-induced silencing-1 (TMS1) cDNA lacking exon2.

SQ Sequence 713 BP; 148 A; 224 C; 223 G; 118 T; 0 other:

Query Match 82.4%; Score 610; DB 22; Length 713;
 Best Local Similarity 92.2%; Pred. No. 6.1e-120;
 Matches 677; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

QY 7 CGGCTGCAGCGGGGTGAGCGGGGCGAGCGGCGGGGATCTTGAGAGCATGGGGCGCGGC 66
 DB 28 CGGCTGCAGCGGGGTGAGCGGGGCGAGCGGCGGGGATCTTGAGAGCATGGGGCGCGGC 87
 QY 67 GCGAGCCATCTTGATGCGCTGAGAACTGACCGCGAGAGGCTCAAGAGTTCAAGC 126
 DB 88 GCGAGCCATCTTGATGCGCTGAGAACTGACCGCGAGAGGCTCAAGAGTTCAAGC 147
 QY 127 TGAAGCTCTGTGGTGGCTGCGCGAGGGCTACGGGGCGCATCCGGGGGCGCGCTGC 186
 DB 148 TGAAGCTCTGTGGTGGCTGCGCGAGGGCTACGGGGCGCATCCGGGGGCGCGCTGC 207
 QY 187 TGTCCATGGAGCCCTTGAGACCTGACGACCAAGCTGTGACCTTCACTGAGACTACG 246
 DB 208 TGTCCATGGAGCCCTTGAGACCTGACGACCAAGCTGTGACCTTCACTGAGACTACG 267
 QY 247 GCGCCGAGCTCACCGCTAAAGTGTGCGGACATGGGCTGCGAGAGATGGCGGGGACG 306
 DB 268 GCGCCGAGCTCACCGCTAAAGTGTGCGGACATGGGCTGCGAGAGATGGCGGGGACG 327

Mon Dec 16 07:22:16 2002

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Page 10

Qy	307	TTGAGGCGGCGCCACGCAACCAGGAGCTTGAGAGCGCGCCAGCTGGGATTCAGAGGCCCTCTC	366
Db	328	TTGAGGCGGCGCCACGCAACCAGGAGCTTGAGAGCGCGCCAGCTGGGATTCAGAGGCCCTCTC	366
Qy	367	AGTCGGCAGCCCAAGCCAGGCTCTGACTTTATAGACCAAGCAGGCGGGCTGGCTTATCCGGA	426
Db	348	-----GGCTGTCACTTTATAGACCAAGCAGGCGGGCTGGCTTATCCGGA	347
Qy	427	GGGTACAAACGTTGAGTGGCTGCTGTGATGCTGTACGGAAGGCTCTGACGATAGC	486
Db	391	GGGTACAAACGTTGAGTGGCTGCTGTGATGCTGTACGGAAGGCTCTGACGATAGC	486
Qy	487	AGTACACAGCAGTGGCGGGCGGACGCCACCAACCCAGCAAGATGGCGAAAGCTCTTCAGTT	546
Db	451	AGTACACAGCAGTGGCGGGCGGACGCCACCAACCCAGCAAGATGGCGAAAGCTCTTCAGTT	546
Qy	547	TCACACACGCTTGGAACCTGACCTGCAGAAAGACTTGTCTCTCCAGGCGCTTAAGGATGCC	606
Db	511	TCACACACGCTTGGAACCTGACCTGCAGAAAGACTTGTCTCTCCAGGCGCTTAAGGATGCC	606
Qy	607	AGGCTTACTGCTGAGAGCACTGTGAGCGAGGAGGCGCTCTCCACGCAAACTCTCGGT	666
Db	571	AGGCTTACTGCTGAGAGCACTGTGAGCGAGGAGGCGCTCTCTCCACGCAAACTCTCGGT	666
Qy	667	CACCGCTTGCAATCCACCAAAATCATCTGAAATCTGATCTTTTATACCAATATACGA	726
Db	631	CACCGCTTGCAATCCACCAAAATCATCTGAAATCTGATCTTTTATACCAATATACGA	726
Qy	727	AAAGCCAGCTTGAA	740
Db	691	AAAGCCAGCTTGAA	704

RESULT 11
 AAH34053
 ID AAH34053 standard; cDNA; 639 bp.
 XX
 AC AAH34053;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1135.
 DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; ss.
 KW
 XX Homo sapiens.
 XX
 XX W0200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 28-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 PR
 DA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 DR WPI: 2001-235357/24.
 DR F-PSDB; AAG74648.
 XX
 PA Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 1; Page 2955; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon

CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in gene
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the activity of P by expressing
 CC Additionally, N may be used to produce the colon cancer-associated Ps.
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC and treatment of colorectal carcinomas and cancers. AA837196 to AA837204
 CC and AA837899 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 CC
 CC Sequence 639 BP; 146 A; 198 C; 189 G; 106 T; 0 other

[illegible]

XX 09-MAR-2001 (first entry)
 XX Human colon cancer antigen nucleotide sequence SEQ ID NO:648.
 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:648.
 XX Human: colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder; ss.
 XX Homo sapiens.
 OS
 PN WO200055351-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000MO-US05883.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-587534/55.
 XX
 DR P-PSDB; AAB53881.
 XX
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 XX
 PS Claim 1; Page 1175; 2104pp; English.
 XX
 XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.
 CC
 XX Sequence 432 BP; 77 A; 142 C; 152 G; 61 T; 0 other;
 XX
 SQ
 Query Match 52.0%; Score 384.6; DB 21; Length 432;
 Best Local Similarity 98.4%; Pred. NO. 2.6e-72;
 Matches 420; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

Db 188 TCATGACGCGCTTGACACTCACCAGCAAGCTGTGACTTCTACTGAGACCTACGGC 247
 QY 249 GCGAGCTCACCGCTTAACGTGTCGCGGACATGGGCTGACAGAGATGGCCGGACGCTG 308
 Db 248 GCGAGCTCACCGCTTAACGTGTCGCGGACATGGGCTGACAGAGATGGCCGGACGCTG 307
 QY 309 CAGGCGGCGACGACGAGGCGCTGAGCGCGGCGACCTGGAGATCCAGGCGCCGCTGACG 368
 Db 308 CAGGCGGCGACGACGAGGCGCTGAGCGCGGCGACCTGGAGATCCAGGCGCCGCTGACG 366
 QY 369 TCGGACGCAAGCGAGGCTGCACTT-ATAGACGACGACGCGGCTGCTTATGCGGAG 427
 Db 367 TCGGACGCAAGCGAGGCTGCACTTATATAGACGACGACGCGGCTGCTG-TTATCGGGA 425
 QY 428 GGTACA 434
 Db 426 GGTCAA 432
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 ID AAD03907 standard; cDNA; 405 BP.
 XX
 AC AAD03907;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Alternatively spliced form of human TMS1 cDNA (lacking exon3).
 XX
 KW Human: target of methylation-induced silencing-1; TMS1; cytostatic;
 KW antiproliferative; apoptosis inducer; gene therapy; CpG island;
 KW caspase-recruiting domain; CARD; cancer; breast; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT CDS 75..404
 FT /*tag= a
 FT /product= "Alternatively spliced form of human TMS1
 FT protein lacking exon3"
 FT /note= "CDS does not include stop codon"
 XX
 PN WO200129235-A2.
 XX
 XX 26-APR-2001.
 PD
 XX
 PF 18-OCT-2000; 2000MO-US28747.
 XX
 PR 18-OCT-1999; 99US-0159975.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Vertino PM;
 XX
 DR WPI; 2001-290922/30.
 DR P-PSDB; AAE00595.
 XX
 PT Novel gene TMS1, transcriptionally silenced due to increased
 PT methylation useful for identifying subject at risk of developing tumor
 PT characterized by abnormal methylation, for treating cancer by inducing
 PT apoptosis -
 XX
 PS Claim 106; Page 123-124; 124pp; English.
 XX
 XX The invention relates to identification of target of methylation-induced
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and
 CC plays a role in induction of apoptosis. TMS1 gene and protein are useful
 CC as tools for diagnosing and treating a subject at risk of developing
 CC cancer (e.g. breast cancer) characterised by abnormal CpG methylation or
 CC abnormally low levels of TMS1 expression products. Unique fragments of

QY 621 GAGACCTGAGCGAGCTGAGCCCTCCACGACACTCGGTGACCCCTGGCAAT 680
 Db 2341 GAGGAGCTGAGCGAGCTGAGCCCTCCACGACACTCGGTGACCCCTGGCAAT 2400
 QY 681 CCCACCAATCATCTGATCTGATCTTTATACACATATACGAAAGCCAGCTTGA 740
 Db 2401 CCCACCAATCATCTGATCTGATCTTTATACACATATACGAAAGCCAGCTTGA 2460

RESULT 15
 AAD03894
 ID AAD03894 standard; DNA; 356 BP.
 AC AAD03894;
 DT 02-JUL-2001 (first entry)
 DE Human target of methylation-induced silencing-1 (TMS1) exon3 DNA.
 OS Homo sapiens.
 KM Human; target of methylation-induced silencing-1; TMS1; cytostatic;
 KW anti-proliferative; apoptosis inducer; gene therapy; CpG island;
 KW caspase-recruiting domain; CARD; cancer; breast; ds.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 3..257
 FT /*tag= a
 FT /product= "Human TMS1 exon3 protein"
 FT /note= "CDS does not include start codon"
 FT /partial

WO200129235-A2.
 XX
 PD 26-APR-2001.
 PF 18-OCT-2000; 2000WO-US28747.
 PR 18-OCT-1999; 99US-0159975.
 PA (UYEM-) UNIV EMORY.
 XX
 PI Vertino PM;
 XX
 DR WPI; 2001-290922/30.
 DR P-PSDB; AAE00591.
 XX
 PT Novel gene TMS1, transcriptionally silenced due to increased
 PT methylation useful for identifying subject at risk of developing tumor
 PT characterized by abnormal methylation, for treating cancer by inducing
 PT apoptosis
 XX
 PS Claim 68; Page 116-117; 124pp; English.
 XX
 CC The invention relates to identification of target of methylation-induced
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and
 CC plays a role in induction of apoptosis. TMS1 gene and protein are useful
 CC as tools for diagnosing and treating a subject at risk of developing
 CC cancer (e.g. breast cancer) characterised by abnormal CpG methylation or
 CC abnormally low levels of TMS1 expression products. Unique fragments of
 CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy.
 CC TMS1 molecule is also useful for treating abnormal cell proliferation by
 CC increasing TMS1 polypeptide level to an above normal level. The CpG
 CC island region of TMS1 or its fragments are used to study the methylation
 CC patterns apart from any coding region contained in it.
 CC The present sequence is human target of methylation-induced silencing-1
 CC (TMS1) exon3 DNA.
 XX
 SQ Sequence 356 BP; 85 A; 108 C; 94 G; 69 T; 0 other;

Query Match 48.1%; Score 356; DB 22; Length 356;
 Best Local Similarity 100.0%; Pred. No. 2.8e-66;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 GCCTGCACTTTATAGACGACACCGGGCTGCGCTTATCGGAGGGTCAACAACTTGAGT 444
 Db 1 GCCTGCACTTTATAGACGACACCGGGCTGCGCTTATCGGAGGGTCAACAACTTGAGT 60
 QY 445 GGCTGCTGATGCTCTGTACGGGAGGCTCTGACGAGTACGACGACGACGAGTGGG 504
 Db 61 GGCTGCTGATGCTCTGTACGGGAGGCTCTGACGAGTACGACGACGACGAGTGGG 120
 QY 505 CGAGGCCAACAACCAAGCAAGATCGGAGGCTCTTCACTTACACCAAGCCTGGAAT 564
 Db 121 CGAGGCCAACAACCAAGCAAGATCGGAGGCTCTTCACTTACACCAAGCCTGGAAT 180
 QY 565 GGACCTGCAAGGACTTGTCTCCAGGCCCTAAGGAGTCCAGTCTACTGTGGAGG 624
 Db 181 GGACCTGCAAGGACTTGTCTCCAGGCCCTAAGGAGTCCAGTCTACTGTGGAGG 240
 QY 625 ACCTGAGCGGAGCTGAGGCTCTTCCAGCAACACTCCGGTACGCGCTGCAATCCA 684
 Db 241 ACCTGAGCGGAGCTGAGGCTCTTCCAGCAACACTCCGGTACGCGCTGCAATCCA 300
 QY 685 CCAATCATCTGATCTGATCTTTATACACATATACGAAAGCCAGCTTGA 740
 Db 301 CCAATCATCTGATCTGATCTTTATACACATATACGAAAGCCAGCTTGA 356

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	740	100.0	740 6	AX082246
2	740	100.0	740 6	AF384665
3	734	99.2	770 6	AX118619
4	734	99.2	770 6	AF184073
5	734	99.2	782 6	AX459863
6	734	99.2	782 6	AB023416
7	734	99.1	779 6	AX017270
8	733	96.4	740 9	AK000211
9	687	92.8	712 9	AF310103
10	680	91.9	772 6	BC013569
11	610	82.4	713 6	AX118641
12	610	82.4	713 6	AF255794
13	585	79.1	585 6	AX082248
14	437.6	59.1	768 9	BC004470
15	378	51.1	405 6	AX118643
16	360	48.6	2821 6	AX118618
17	360	48.6	2821 9	AF184072
18	360	48.6	23305 9	AC009088
19	356	48.1	356 6	AX118626
20	336	45.4	732 10	BC008252
21	336	45.4	770 10	AB032249
22	336	45.4	777 6	AX082258
23	336	45.0	803 6	AX118637
24	322	43.5	626 6	AX118621
25	321	42.7	579 6	AX082260
26	316.2	41.9	321 6	AX084819
27	309.8	37.4	605 6	AX118639
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35	174.4	23.6	587 9	AF454669
36	174.4	23.6	807 6	AX048091
37	174.4	22.9	270 6	AX417218
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39	166	22.4	168975 2	AC106629
40	129	17.4	52521 2	AC102309
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ALIGNMENTS

RESULT 1
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LOCUS AX082246 740 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 48 from Patent WO0100826.
ACCESSION AX082246
VERSION AX082246.1 GI:13171007
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Bertin, J.
TITLE Novel molecules of the card-related protein family and uses thereof
JOURNAL Patent: WO 0100826-A 48 04-JAN-2001;

Mon Dec 16 07:22:15 2002

us-09-728-721-48.rge

FEATURES Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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CDS 54..641
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BASE COUNT 146 a 236 c 236 g 120 t
ORIGIN

Query Match 100.0% Score 740; DB 6; Length 740;
Best Local Similarity 100.0%; Pred. No. 2.5e-107;
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DB 1 CGCGTCCGGCTGAGCGGGGTGAGCGCGCGCGGAGATCTGAGCCATGGGCG 60
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DB 61 GCGCGCGGAGCGCATCTCTGAGTGGCGTGAAGAACCTGACCGCGGAGAGCTCAAGAACT 120
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OY 721 ATACGAAAGACGCTTGA 740
DB 721 ATACGAAAGACGCTTGA 740

RESULT 2 AF384665 740 bp mRNA linear PRI 19-JUN-2001
LOCUS AF384665
DEFINITION Homo sapiens caspase recruitment domain protein 5 mRNA, complete cds.
ACCESSION AF384665
VERSION AF384665.1 GI:1448058
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS Bertin,J.
TITLE CARD5 Protein is a CARD/PYRIN family member that is involved in apoptosis signal transduction
JOURNAL Unpublished
AUTHORS Bertin,J.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-2001) Neurobiology, Millennium Pharmaceuticals Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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54..641
/note="CARD5; CARD/PYRIN family member; bipartite protein comprised of an N-terminal PYRIN domain and a C-terminal CARD domain; Involved in apoptosis signal transduction"
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ORIGIN

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Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CGCGTCCGGCTGAGCGGGGTGAGCGCGCGCGGAGATCTGAGCCATGGGCG 60
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QY	421	TCGAGGGGTCAACAACGTTGAGTGTGCTGCTGCTGATGCTCTGTGACGGGAAGGCTCTGACGG	480
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QY	661	TCGCGTCAAGCCCTTGCAATCCACCAATATCATCTGATCTGATCTTTTATACAAAT	720
Db	661	TCGCGTCAAGCCCTTGCAATCCACCAATATCATCTGATCTGATCTTTTATACAAAT	720
Y	721	ATACGAAAAGCCAGCTTGAA 740	
Db	721	ATACGAAAAGCCAGCTTGAA 740	
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DEFINITION	Sequence 2 from Patent WO0129235.		linear
ACCESSION	AX118619		
VERSION	AX118619.1	GI:14035570	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 770)		
JOURNAL	Tmsi compositions and methods of use		
FEATURES	Patent: WO 0129235-A 2 26-Apr-2001;		
source	Emory University (US)		
	location/Qualifiers		
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	Query Match	99.2%; Score 734;	DB 6; Length 770;
	Best Local Similarity	100.0%;	Pred. No. 2, 2e-106;
	Matches 734;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	7	CGGCGCAGCGGGGGGAGCAGCGGCGAGGCGGGGATCTGAGACCTATGGGCGCGCGC	66
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QY	67	GCGAGCCATCTGGATCGCTGGGAGAACCTGACCGCGAGAGCTCAAGAATTCACAGC	126
Db	88	GCGAGCCATCTGGATCGCTGGGAGAACCTGACCGCGAGAGCTCAAGAATTCACAGC	147
QY	127	TGAAGCTCTGTGCTGCTCGCTCGCTGCGCGAGGGCTACAGGGGCGATCCCGGGGGCGGCTGC	186
Db	148	TGAAGCTCTGTGCTGCTCGCTCGCTGCGCGAGGGCTACAGGGGCGATCCCGGGGGCGGCTGC	207

QY	187	TGTCATGAGCGCTTTGGACCTTACCAGCAAGCTGGTGACTTTCATTACCTGTGAGACTACG	246
Db	208	TGTCCATGGAGGCCCTTGGACCTCACCGACAACACTGGTAGCTTCTAACCTGTGAGACTACG	267
QY	247	GCGCGCAGCTACCGCTTAACGTCTGCGCGGACATGGGCTGTGACGAGATATGGCCGGGCAGC	306
Db	268	GCGCGCAGCTACCGCTTAACGTCTGCGGACATGGGCTGTGACGAGATATGGCCGGGCAGC	327
QY	307	TTCAGGCGGCCACGACACGAGGGCTGTGAGCGCGCCAGCTGGAGATCCAGGCCCCCTC	366
Db	328	TTCAGGCGGCCACGACACGAGGGCTGTGAGCGCGCCAGCTGGAGATCCAGGCCCCCTC	387
QY	367	AAGTCGACGCCAAGCCAGGCTGTCACTTTATATAGACCAGCAGCCGGCTGCTTATCGGA	426
Db	388	AAGTCGACGCCAAGCCAGGCTGTCACTTTATATAGACCAGCAGCCGGCTGCTTATCGGA	447
QY	427	GGGTCAAAACCTGTGATGGCTGCTGAGATGCTGTATAGCGGAAGGTCCTGACGAGTATGAC	486
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QY	487	AGTACGAGCAGTGGCGGCCGAGCCACCACCAAGCAAGATGGCGAAGCTTTCAGTT	546
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QY	547	TCACACAGACCTTGGAACTGTGACCTGTGACAGGACTTGTCTCCAGGCCCATAAGGAGTCCC	606
Db	568	TCACACAGACCTTGGAACTGTGACCTGTGACAGGACTTGTCTCCAGGCCCATAAGGAGTCCC	627
QY	607	AGTCCACTGCTGGTGAGGACCTGTGAGCGGAGTGTGAGGCTCTTCCAGCAACATCCGGT	666
Db	628	AGTCCACTGCTGGTGAGGACCTGTGAGCGGAGTGTGAGGCTCTTCCAGCAACATCCGGT	687
QY	667	CAGCCCTTGGCAATCCACCAAATCATCTGTAATCTTATATACAAATATAGA	726
Db	688	CAGCCCTTGGCAATCCACCAAATCATCTGTAATCTTATATACAAATATAGA	747
QY	727	AAAGCAGCTTGAA	740
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DEFINITION	Homo sapiens target of methylation-induced silencing 1 (TMS1) mRNA,		
	complete cds.		
ACCESSION	AF184073		
VERSION	AF184073.1	GI:9863863	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 770)		
AUTHORS	Conway,K.E., McConnell,B.B., Bowring,C.E., Donald,C.D., Warren,S.T.		
	and Vertino,P.M.		
TITLE	TMS1, a novel proapoptotic caspase recruitment domain protein, is a		
	target of methylation-induced gene silencing in human breast		
	cancers		
JOURNAL	Cancer Res. 60 (22), 6236-6242 (2000)		
MEDLINE	20552139		
PUBMED	11103776		
REFERENCE	2 (bases 1 to 770)		
AUTHORS	McConnell,B.B. and Vertino,P.M.		
TITLE	Activation of a caspase-9-mediated apoptotic pathway by subcellular		
	distribution of the novel caspase recruitment domain protein TMS1		
JOURNAL	Cancer Res. 60 (22), 6243-6247 (2000)		
MEDLINE	20552140		
PUBMED	11103777		
REFERENCE	3 (bases 1 to 770)		
AUTHORS	Vertino,P.M.		
TITLE	Direct Submission		

JOURNAL		Submitted (09-SEP-1999) Radiation Oncology, Emory University School of Medicine, 145 Edgewood Avenue, SE, Atlanta, GA 30335, USA	
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BASE COUNT		157 a 247 c 241 g 125 t	
ORIGIN			
Query Match		99.28; Score 734; DB 9; Length 770;	
Best Local Similarity		100.0%; Pred. No. 2.2e-106;	
Matches 734; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
OY	7	CGCGTCGACGCGGGGTGAGCGCGCGAGCGCGGGGATCTTGAGCCATGGGGCGCGC	66
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OY	67	GCGAGCCATCTTGAGTGGCTGAGACCTGACCGCGAGAGCTCAAGAGTTCAAGC	126
DB	88	GCGAGCCATCTTGAGTGGCTGAGACCTGACCGCGAGAGCTCAAGAGTTCAAGC	147
OY	127	TGAAGCTGCTGCTGGTGGCGGCTGCGGAGGCTACGGGCGCATCCCGGGGCGCGTGC	186
DB	148	TGAAGCTGCTGCTGGTGGCGGCTGCGGAGGCTACGGGCGCATCCCGGGGCGCGTGC	207
OY	187	TGTCCATGAGCGGCTTGACCTGACCGACCAAGCTGCTGACCTTCTACCTGAGACCTAGC	246
DB	208	TGTCCATGAGCGGCTTGACCTGACCGACCAAGCTGCTGACCTTCTACCTGAGACCTAGC	267
OY	247	GCGCGAGCTCAACCGCTTAACGCTGCTGCGGACATGGGCTGCAAGAGATGGCGGCAAGC	306
DB	268	GCGCGAGCTCAACCGCTTAACGCTGCTGCGGACATGGGCTGCAAGAGATGGCGGCAAGC	327
OY	307	TGAGAGCGGCGACGACCAAGGCTCTGAGGCGCGGCGGACGCTGGAGTCAGAGCCCTCTGC	366
DB	328	TGAGAGCGGCGACGACCAAGGCTCTGAGGCGCGGCGGACGCTGGAGTCAGAGCCCTCTGC	387
OY	367	AGTGGGACGCCAAGCGAGGCTGCACTTTATAGACAGCACCGGGTGGCGTTATCGGCA	426
DB	388	AGTGGGACGCCAAGCGAGGCTGCACTTTATAGACAGCACCGGGTGGCGTTATCGGCA	447
OY	427	GGGTCACAAAGCTTGAAGTGGCTGCTGATCTGTACGAGGAGGTCGACGAGTGAAGC	486
DB	448	GGGTCACAAAGCTTGAAGTGGCTGCTGATCTGTACGAGGAGGTCGACGAGTGAAGC	507
OY	487	AGTACAGGAGCTGGGGCGGAGGCCACCAACCAAGCAAGATGGGAAAGCTCTTCAGTT	546
DB	508	AGTACAGGAGCTGGGGCGGAGGCCACCAACCAAGCAAGATGGGAAAGCTCTTCAGTT	567
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DB	568	TGACACGAGCTGGAGACCTGCAAGAGACTTGTCTCCAGGCGCTTAAGGAGTCCG	627
OY	607	AGTCTACCTGCTGGAGGAGCTGAGAGGCTCTCTCCACCAACACTCCGGT	666

DB	628	AGTCTACCTGCTGGAGGAGCTGAGAGGCTCTCTCCACCAACACTCCGGT	687
OY	667	CAGCCCTGGCAATCCGACCAATGCAATGCTGATCTTTTATACCAATATAGCA	726
DB	688	CAGCCCTGGCAATCCGACCAATGCAATGCTGATCTTTTATACCAATATAGCA	747
OY	727	AAAGCCAGCTTGAA	740
DB	748	AAAGCCAGCTTGAA	761

RESULT 5		AX459863	
LOCUS		AX459863	
DEFINITION		Sequence 6 from Patent WO0240668.	
ACCESSION		AX459863.1	
VERSION		GI:21725640	
KEYWORDS		human.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
AUTHORS		Tschopp, J. and Martignon, F.	
TITLE		Proteins and dna sequences underlying these proteins used for treating inflammations	
JOURNAL		Patent; WO 0240668-A 6 23-MAY-2002;	
FEATURES		Apotech Research and Development Ltd. (CH)	
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OY	67	GCGAGCCATCTTGAGTGGCTGAGACCTGACCGCGAGAGCTCAAGAGTTCAAGC	126
DB	100	GCGAGCCATCTTGAGTGGCTGAGACCTGACCGCGAGAGCTCAAGAGTTCAAGC	159
OY	127	TGAAGCTGCTGCTGGTGGCGGCTGCGGAGGCTACGGGCGCATCCCGGGGCGCGTGC	186
DB	160	TGAAGCTGCTGCTGGTGGCGGCTGCGGAGGCTACGGGCGCATCCCGGGGCGCGTGC	219
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DB	220	TGTCCATGAGCGGCTTGACCTGACCGACCAAGCTGCTGACCTTCTACCTGAGACCTAGC	279
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DB	280	GCGCGAGCTCAACCGCTTAACGCTGCTGCGGACATGGGCTGCAAGAGATGGCGGCAAGC	339
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DB	340	TGAGAGCGGCGACGACCAAGGCTCTGAGGCGGCGGACGCTGGAGTCAGAGCCCTCTGC	399
OY	367	AGTGGGACGCCAAGCGAGGCTGCACTTTATAGACAGCACCGGGTGGCGTTATCGGCA	426
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RESULT 6
AB023416 782 bp mRNA linear PRI 18-OCT-2000
LOCUS Homo sapiens ASC mRNA for apoptosis-associated speck-like protein
DEFINITION containing a CARD, complete cds.
ACCESSION AB023416
VERSION AB023416.2 GI:10801601
KEYWORDS ASC.
SOURCE Homo sapiens CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Masumoto, J., Taniguchi, S., Ayukawa, K., Sarvotham, H., Kishino, T.,
Nikawa, N., Hidaka, E., Katsuyama, T., Higuchi, T. and Sagara, J.
TITLE A novel 22-kDa protein, aggregates during apoptosis of human
promyelocytic leukemia HL-60 cells
J. Biol. Chem. 274 (48), 33835-33838 (1999)
JOURNAL
MEDLINE 20036508
REFERENCE 2 (bases 1 to 782)
AUTHORS Masumoto, J., Sagara, J. and Taniguchi, S.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1999) Junya Masumoto, Shinshu University School
of Medicine, Research Center on Aging and Adaptation, Asahi 3-1-1,
Matsumoto, Nagano 390-8621, Japan
(E-mail: masumoto@sch.md.shinshu-u.ac.jp, Tel: 81-263-37-2723,
Fax: 81-263-37-2724)
COMMENT On Oct 14, 2000 this sequence version replaced gi:6482371.
Sequence updated (29-Nov-1999).
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BASE COUNT 158 a 251 c 246 g 127 t
Query Match 99.2%; Score 734; DB 9; Length 782;

Best Local Similarity 100.0%; Pred. No. 2,2e+106;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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LOCUS Sequence 21 from Patent WO947669.
DEFINITION AX017270
ACCESSION AX017270
VERSION AX017270.1 GI:10042188
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and
Pilarczyk, C.
TITLE Human nucleic acid sequences from tissue of breast tumors
JOURNAL Patent: WO 947669-A 21 23-SEP-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN

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 LOCUS Homo sapiens PYCARD mRNA, complete cds.
 DEFINITION AF310103.1 GI:11096298
 ACCESSION AF310103.1 GI:11096298
 VERSION AF310103.1 GI:11096298
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Martinon,F., Hofmann,K. and Tschopp,J.
 TITLE The Pyrin domain: a possible member of the death domain-fold family
 implied in apoptosis and inflammation
 JOURNAL Curr. Biol. 11 (4), R118-R120 (2001)
 MEDLINE 21148093
 PUBMED 11250163
 REFERENCE
 PUBLISHED 2 (bases 1 to 712)
 AUTHORS Martinon,F., Hofmann,K. and Tschopp,J.
 TITLE Direct Submission
 JOURNAL Submitted (28-SEP-2000) Institute of Biochemistry, University of
 Lausanne, CH des Boveresses 155, Epalinges 1066, Switzerland
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 BASE COUNT 166 a 221 c 210 g 115 t
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Query Match 92.8%; Score 687; DB 9; Length 712;
 Best Local Similarity 100.0%; Pred. No. 5,7e-99;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 534 AAGCTCTTCACTTTCACACACAGCTGGAACCTGACCTGCAAGAGAGAGAGAGAG 593
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 Db 481 AAGCTCTTCACTTTCACACACAGCTGGAACCTGACCTGCAAGAGAGAGAGAGAG 540
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 QY 654 GCACACTCCGCGTCCAGGCGCTGCAATCCCAACCAATCATCTGATCTTTTAT 713
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 Db 601 GCACACTCCGCGTCCAGGCGCTGCAATCCCAACCAATCATCTGATCTTTTAT 660
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 QY 714 ACACATATACGAAAGCCAGCTTGAA 740
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 Db 661 ACACATATACGAAAGCCAGCTTGAA 687
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 RESULT 10
 BC013569 772 bp mRNA linear PRI 29-OCT-2001
 LOCUS BC013569
 DEFINITION Homo sapiens, apoptosis-associated speck-like protein containing a
 CARD, clone MGC:8873 IMAGE:3902319, mRNA, complete cds.
 ACCESSION BC013569
 VERSION BC013569.1 GI:15488878
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (04-SEP-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK
 COMMENT NIH-MGC Project URL: http://mgc.ncl.nih.gov
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.

cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mdickpaxil@stanford.edu
Dickson, M., Schmitz, J., Grimwood, J., Kodrzycki, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAC Plate: 14 Row: 9 Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7020146.
Location/Qualifiers

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CDS

BASE COUNT 232 a 220 c 206 g 114 t
ORIGIN

Query Match Best Local Similarity 91.9%; Score 680; DB 9; Length 772;
Matches 680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCGCGGCGAGCCATCTGTGATGCGTGGAGAACCTGACCGCGGAGGCTCAAGAGT 60
OY 121 TCAAGCTGAAGTGTGTGCTGCGCGCGGAGGCTCAAGGCGCATCCCGGGGCG 180
DB 61 TCAAGCTGAAGTGTGTGCTGCGCGCGGAGGCTCAAGGCGCATCCCGGGGCG 120
OY 181 CGCTGCTGCCATGAGCGCCTTGAGCTCAACGCAAGCTGCTTCACTGAGAGA 240
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OY 241 CCTACGGGCGGAGCTCAACGCTTACGCTGCGGACATGGGCTTCAAGAGATGCGG 300
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OY 421 TCGGAGGCTGACAAAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGAGG 480
DB 361 TCGGAGGCTGACAAAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGAGG 420
OY 481 ATGAGCAATGACGAGGCTGAGGCGGAGGCTGAGGCGGCGGCTGAGATCCAGGCC 540
DB 421 ATGAGCAATGACGAGGCTGAGGCGGAGGCTGAGGCGGCGGCTGAGATCCAGGCC 480
OY 541 TCAGTTTCAACAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGG 600

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OY 661 TCGGTCACGCGGCTGAGTGTGAGGAGCTGAGGCGGAGGCTGAGTGTGAGGAGT 720
DB 601 TCGGTCACGCGGCTGAGTGTGAGGAGCTGAGGCGGAGGCTGAGTGTGAGGAGT 660
OY 721 ATACGAAAGGAGGCTGAGT 740
DB 661 ATACGAAAGGAGGCTGAGT 680

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RESULT 11

AX118641

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

BASE COUNT

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Query Match Best Local Similarity 82.4%; Score 610; DB 6; Length 713;
Matches 677; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

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OY 67 GCGAGCGCATCTGATGTGCGTGTGAGAGCTGACCGCGGAGGAGCTCAAGAGTTCAAGC 126
DB 88 GCGAGCGCATCTGATGTGCGTGTGAGAGCTGACCGCGGAGGAGCTCAAGAGTTCAAGC 147
OY 127 TGAAGCTGTGTGCGTGTGCGGCTGCGCGAGGCGCTACGCGGCGGAGCTCAAGAGTTCAAGC 186
DB 148 TGAAGCTGTGTGCGTGTGCGGCTGCGCGAGGCGCTACGCGGCGGAGCTCAAGAGTTCAAGC 207
OY 187 TGTCCATGTGAGGCGCTGTGAGAGCTGACCGAGGCTGACCTTCACTGAGGAGCTCAAGC 246
DB 208 TGTCCATGTGAGGCGCTGTGAGAGCTGACCGAGGCTGACCTTCACTGAGGAGCTCAAGC 267
OY 247 GCGCGAGCTACCGCTTAAGCTGTGCGGCGGAGGCTGAGGCGGAGGAGTGTGCGGCGGAGC 306
DB 268 GCGCGAGCTACCGCTTAAGCTGTGCGGCGGAGGCTGAGGCGGAGGAGTGTGCGGCGGAGC 327
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Db 328 TGCAGCGCGCCAGCACAG----- 347

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Db 348 -----GGCCTGCACTTTATACACAGCAGCCGGCTGCGCTTATCGCA 390

QY 427 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTATACGGGAGGTCCTGACGGATGAG 486

Db 391 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTATACGGGAGGTCCTGACGGATGAG 450

QY 487 AGTACGAGCAGTGCAGGCGGAGCCACCAACCAAGATGCGAGCTTTCAGTT 546

Db 451 AGTACGAGCAGTGCAGGCGGAGCCACCAACCAAGATGCGAGCTTTCAGTT 510

QY 547 TCACACAGCCTGGAACCTGAGCTGCAAGACTTCTCTCCAGGCGCTTAAGGAGTCC 606

Db 511 TCACACAGCCTGGAACCTGAGCTGCAAGACTTCTCTCCAGGCGCTTAAGGAGTCC 570

QY 607 AGTCTACCTGCTGGAGGAGCTGAGCGGAGCTGAGGCTCTCCAGCAACCTCGGT 666

Db 571 AGTCTACCTGCTGGAGGAGCTGAGCGGAGCTGAGGCTCTCCAGCAACCTCGGT 630

QY 667 CAGCCCTGCGCAATCCACCAATCATCTGATCTTTTATACAAATATACGA 726

Db 631 CAGCCCTGCGCAATCCACCAATCATCTGATCTTTTATACAAATATACGA 690

QY 727 AAGCCAGCTTGAA 740

Db 691 AAGCCAGCTTGAA 704

RESULT 12

AP255794 713 bp mRNA linear PRI 02-FEB-2001

LOCUS AF255794 Homo sapiens target of methylation-induced silencing-1 (TMS1) mRNA, complete cds, alternatively spliced.

ACCESSION AF255794

VERSION AF255794.1 GI:9802275

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 713)

AUTHORS Conway,K.E., McConnell,B.B., Bowring,C.E., Donald,C.D., Warren,S.T., and Vertino,P.M.

TITLE TMS1, a novel proapoptotic caspase recruitment domain protein, is a target of methylation-induced gene silencing in human breast cancers

JOURNAL Cancer Res. 60 (22), 6243-6247 (2000)

REFERENCE 2 (bases 1 to 713)

AUTHORS McConnell,B.B., and Vertino,P.M.

TITLE Activation of a caspase-9-mediated apoptotic pathway by subcellular redistribution of the novel caspase recruitment domain protein TMS1

JOURNAL Cancer Res. 60 (22), 6243-6247 (2000)

PUBMED 11103777

REFERENCE 3 (bases 1 to 713)

AUTHORS Vertino,P.M.

TITLE Direct Submission

JOURNAL Submitted (13-APR-2000) Radiation Oncology, Emory University School of Medicine, 145 Edgewood Avenue, SE, Atlanta, GA 30335, USA

FEATURES

source location/Qualifiers

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CDS

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BASE COUNT 148 a 224 c 223 g 118 t

ORIGIN

Query Match 82.4%; Score 610; DB 9; Length 713;

Best Local Similarity 92.2%; Pred. No. 7, 8e-87;

Matches 677; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

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QY 67 GCGAGCCATCTCGATGCGCTGAGAACCTGACCCCGAGAGCTCAAGAAATTCAAG 126

Db 88 GCGAGCCATCTCGATGCGCTGAGAACCTGACCCCGAGAGCTCAAGAAATTCAAG 147

QY 127 TGAAGCTGCTGTGCGTGCCTGCGGAGGCTACGAGGCGCATCCGCGGGCGCGTGC 186

Db 148 TGAAGCTGCTGTGCGTGCCTGCGGAGGCTACGAGGCGCATCCGCGGGCGCGTGC 207

QY 187 TGTTCATGAGAGCGCTTGAGCTCAGCAGCAAGTGTGACCTTACCTGGAACCTACG 246

Db 208 TGTTCATGAGAGCGCTTGAGCTCAGCAGCAAGTGTGACCTTACCTGGAACCTACG 267

QY 247 GCGCGAGCTCACCGCTTAACGTCTGCGGACATGGGCGCTGAGAGATGGCGGCGAGC 306

Db 268 GCGCGAGCTCACCGCTTAACGTCTGCGGACATGGGCGCTGAGAGATGGCGGCGAGC 327

QY 307 TGGAGCGGCGCACAGCACAGGCGCTGTGAGCGCGCCAGCTGGGATCCAGCCCTCTC 366

Db 328 TGCAGCGCGGCACGACACAG----- 347

QY 367 AGTCGGCAGCCAGCAGCGCTCTATTATACAGCAGCCGGCTGCGCTTATCGCA 426

Db 348 -----GGCCTGCACTTTATACACAGCAGCCGGCTGCGCTTATCGCA 390

QY 427 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTATACGGGAGGTCCTGACGGATGAG 486

Db 391 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTATACGGGAGGTCCTGACGGATGAG 450

QY 487 AGTACGAGCAGTGCAGGCGGAGCCACCAACCAAGATGCGAGCTTTCAGTT 546

Db 451 AGTACGAGCAGTGCAGGCGGAGCCACCAACCAAGATGCGAGCTTTCAGTT 510

QY 547 TCACACAGCCTGGAACCTGAGCTGCAAGACTTCTCTCCAGGCGCTTAAGGAGTCC 606

Db 511 TCACACAGCCTGGAACCTGAGCTGCAAGACTTCTCTCCAGGCGCTTAAGGAGTCC 570

QY 607 AGTCTACCTGCTGGAGGAGCTGAGCGGAGCTGAGGCTCTCCAGCAACCTCGGT 666

Db 571 AGTCTACCTGCTGGAGGAGCTGAGCGGAGCTGAGGCTCTCCAGCAACCTCGGT 630

QY 667 CAGCCCTGCGCAATCCACCAATCATCTGATCTTTTATACAAATATACGA 726

Db 631 CAGCCCTGCGCAATCCACCAATCATCTGATCTTTTATACAAATATACGA 690

QY 727 AAGCCAGCTTGAA 740

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Db      691  |||||||||||
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RESULT 13
LOCUS   AX082248
DEFINITION Sequence 50 from Patent WO0100826.
ACCESSION AX082248
VERSION   AX082248.1 GI:13171009
KEYWORDS
SOURCE   human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    Bertin, J.
JOURNAL  Novel molecules of the card-related protein family and uses thereof
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BASE COUNT 111 a 188 c 195 g 91 t
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Best Local Similarity 100.0%; Pred. No. 6.9e-83;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 ATGGGGCGCGCGCGCGCGCGCATCTGATGCGCTGAGAACTGACCGCGAGAGCTC 113
Db 1 ATGGGGCGCGCGCGCGCGCGCATCTGATGCGCTGAGAACTGACCGCGAGAGCTC 60
OY 114 AAGAAGTTCAAGCTGAAGCTGCTGTGCGCGCTGCGCGAGGCGCTACGGGCGCATCCG 173
Db 61 AAGAAGTTCAAGCTGAAGCTGCTGTGCGCGCTGCGCGAGGCGCTACGGGCGCATCCG 120
OY 174 CGGGGCGCGCTGCTGCTCATGAGACGCGCTTGACCTACCGAGAGCTGCTCAGCTTCTAC 233
Db 121 CGGGGCGCGCTGCTGCTCATGAGACGCGCTTGACCTACCGAGAGCTGCTCAGCTTCTAC 180
OY 234 CTGGAGACTAGAGCGCGCGCGAGCTCACCGCTTAACGTGCTGCGCGAGATGGGCTGACAGAG 293
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OY 294 ATGGCGGGGAGCTGAGCGCGCGCGAGCGAGCGGCTCTGAGCGCGCGCGAGCTGGAGTC 353
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OY 354 CAGGCCCTCTCTCAGTGGCGAGCGCAAGCCAGGCTGCACTTTATAGACAGCAACGGGCT 413
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OY 414 GCGCTTATCGCGAGGCTCAAAACGTTGAGTGGCTGCTGATGCTGTACGGGAGAGTC 473
Db 361 GCGCTTATCGCGAGGCTCAAAACGTTGAGTGGCTGCTGATGCTGTACGGGAGAGTC 420
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Db 421 CTGAGGAGTAGAGTAGAGTAGAGTAGAGCGAGCGAGCGCAACCAACCAAGATAGCGG 480
OY 534 AAGCTTTCAGTTTTCACACCAAGCTGGAACCTGCAAGAGCTTGTCTCCAGGCGC 593
Db 481 AAGCTTTCAGTTTTCACACCAAGCTGGAACCTGCAAGAGCTTGTCTCCAGGCGC 540
OY 594 CTAAGGAGTCCAGTCTTACTGCTGAGAGAGCTGAGAGCGGAGC 638
Db 541 CTAAGGAGTCCAGTCTTACTGCTGAGAGAGCTGAGAGCGGAGC 585

RESULT 14

BC004470
LOCUS   BC004470
DEFINITION Homo sapiens, clone MGC:10332 IMAGE:3678925, mRNA, complete cds.
ACCESSION BC004470
VERSION   BC004470.1 GI:13325315
KEYWORDS
SOURCE   MGC.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    Strausberg, R.
JOURNAL  Direct Submission
          Submitted (12-MAR-2001) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
          NIH-MGC Project URL: http://mgc.nci.nih.gov
          Contact: MGC help desk
          Email: cgaphs-remail.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
          CDNA Library Preparation: Rubin Laboratory
          DNA Sequencing by: Institute for Systems Biology
          http://www.systemsbio.org
          Contact: amadensystemsbio.org
          Anup Madan, Rachel Dickhoff, Jessica Fahy, Stephanie Ford, Julia
          Greene, Mark Kettelman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRML Plate: 14 Row: 9 Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10801601.

FEATURES
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BASE COUNT 168 a 229 c 256 g 115 t
ORIGIN

Query Match      59.1%; Score 437.6; DB 9; Length 768;
Best Local Similarity 91.3%; Pred. No. 1.1e-59;
Matches 464; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 233 CCTGGAGACTAGAGCGCGCGAGCTGACCGCTTAACGTGCTGCGCGAGATGGGCTGACAGA 292
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OY 293 GATGGCGGGGCGCGCGCGCGCGAGCGCGAGCGGCTCTGAGCGCGCGCGAGCTGGGAT 352
Db 305 CAAGAAGTTCAAGCTGAGCGCGCGCGCGAGCGGCTCTGAGCGCGCGCGAGCTGGGAT 364
OY 353 CCAGGCCCTCTCTCAGTGGCGAGCGCAAGCCAGGCTGCACTTTATAGACAGCAACGGGCG 412
Db 365 CCAGGCCCTCTCTCAGTGGCGAGCGCAAGCCAGGCTGCACTTTATAGACAGCAACGGGCG 424
OY 413 TGCCTTATCGCGAGGCTCAAAACGTTGAGTGGCTGCTGATGCTGTACGGGAGAGT 472
Db 425 TGCCTTATCGCGAGGCTCAAAACGTTGAGTGGCTGCTGATGCTGTACGGGAGAGT 484

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Best Local Similarity	99.7%;	Pred. 1.8e-143;			
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OY	69	GACCCATCTCGATGATGGCGGTGAGAGACCTGACCGCCGAGGAGAGCTCAAGAGTTCACACTG	128		
Db	61	GACCCATCTCGATGATGGCGGTGAGAGACCTGACCGCCGAGGAGAGCTCAAGAGTTCACACTG	120		
OY	129	AAGTGTGTGTCGGTGGCGGTGCGCGAGGGCTCTAGGGGCCATTCGCCGGGGCGGCTCTG	188		
Db	121	AAGTGTGTGTCGGTGGCGGTGCGCGAGGGCTCTAGGGGCCATTCGCCGGGGCGGCTCTG	180		
OY	189	TCCATGAGACGGCTTGGAGCTCAGCGAGAGCTGTACACTTCTACTGAGAGACCTTACAGGC	248		
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OY	249	GCCAGCTCACCCTTAACGTGCTGCGCGCATGAGGGCTCTGAGAGAGATGGCGGCGACCTG	308		
Db	241	GCCAGCTCACCCTTAACGTGCTGCGCGCATGAGGGCTCTGAGAGAGATGGCGGCGACCTG	300		
OY	309	CAGGCGGCGACAGCCAGGGCTCTGGAGCGCGGCGACAGCTGGAGATCCAGAGCCCTCTCAG	368		
Db	301	CAGGCGGCGACAGCCAGGGCTCTGGAGCGCGGCGACAGCTGGAGATCCAGAGCCCTCTCAG	360		
OY	369	TGGGACACCAAGCCAGGCTCTGCACTTTATAGACCAAGCCAGGGCTGGGCTTATGCGAGG	428		
Db	361	TGGGACACCAAGCCAGGCTCTGCACTTTATAGACCAAGCCAGGGCTGGGCTTATGCGAGG	420		
OY	429	GTCACAAACCTTATAGTGGCTGCTGGATGCTCTGTACGGGAAGATGTCAGAGATGAGACAG	488		
Db	421	GTCACAAACCTTATAGTGGCTGCTGGATGCTCTGTACGGGAAGATGTCAGAGATGAGACAG	480		
OY	489	TACAGGACATGGGGGCGCGGCGACCAACCAACCAACAGATGCGGAAGCTCTTACAGTTTC	548		
Db	481	TACAGGACATGGGGGCGCGGCGACCAACCAACCAACAGATGCGGAAGCTCTTACAGTTTC	540		
OY	549	ACACCACTCTGGAATGAGACTCTGCAAGAGACTGCTCTCCAGAGCCCTTAAGGAGATCCCA	608		
Db	541	ACACCACTCTGGAATGAGACTCTGCAAGAGACTGCTCTCCAGAGCCCTTAAGGAGATCCCA	600		
OY	609	TCTTACCTGGTGGAGGAGCTGGAGCGGAGAGCTGAGGCTCTTCCAGCAACACCTCGGTCA	668		
Db	601	TCTTACCTGGTGGAGGAGCTGGAGCGGAGAGCTGAGGCTCTTCCAGCAACACCTCGGTCA	660		
OY	669	GGCGGTGGCAATCCCAACCAATATCTGTAATCTTTTATACCAATATAGCAAA	728		
Db	661	GGCGGTGGCAATCCCAACCAATATCTGTAATCTTTTATACCAATATAGCAAA	720		
OY	729	AGCCAGCTTGA	740		
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[illegible]

Db	367	TCATCGGGACCAACGACCGGCTCTGCACTTTATATAGACGACACCGGGCTGGCGTTATGCG	426
Qy	425	GAGGGTCACAAACGTTGAGTGGCTGCTGGAGATGCTCTGTACGGGAAGGTCGTGACGGATGA	484
Db	427	GAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCGTGACGGATGA	486
Qy	485	GCAGTACCAAGCAGTGGCGGGCCGAGCCACCAACCCAAAGCANAATGCGGAAGCTTTAG	544
Db	487	GCAGTACCAAGCAGTGGCGGGCCGAGCCACCAACCCAAAGCANAATGCGGAAGCTTTAG	546
Qy	545	TTTGACACCACTGGGAAGCTGGACCTGGCAAGACTGGTCTCCGACGGCCCTAAGGGAATC	604
Db	547	TTTGACACCACTGGGAAGCTGGACCTGGCAAGACTGGTCTCCGACGGCCCTAAGGGAATC	606
Qy	605	CCAGTCTTACTGGTGGAGACCTGGAGCGAGCTGAGAGCTTCCTCCAGCAACACTCGG	664
Db	607	CCAATCTTACTGGTGGAGACCTGGAGCGAGCTGAGAGCTTCCTCCAGCAACACTCGG	666
Qy	665	GTCAGCCCCCTGGCAATCCACCAAAATCTATCTGAATCTGATCTTTTATACAAATATAC	724
Db	667	GTCAGCCCCCTGGCAATCCACCAAAATCTATCTGAATCTGATCTTTTATACAAATATAC	726
Qy	725	GAAAGCCAGCTTGAA 740	
Db	727	GAAAGCCAGCTTGAA 742	

RESULT 3					
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LOCUS	BM10918	767 bp	mRNA	linear	EST 12-MAR-2002
DEFINITION	AEENCOURT_6615922 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5454497				
	5', mRNA sequence.				

ACCESSION	BM910918
VERSION	BM910918.1
KEYWORDS	EST.
SOURCE	human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
REFERENCE NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LNCM1949 row: 1 column: 18
High quality sequence stop: 641.
Location/Qualifiers
1. .767

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/clone_1id="NIH_MGC_98"
/tissue_type="astrocytoma grade IV, cell line"
/lab_host="DHI0B (phage-resistant)"
/note="Organ: brain; Vector: pOTB1; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAC(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH_MGC Library."

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Query Match	97.6%;	Score 722;	DB 14;	Length 767;
Best Local Similarity	99.7%;	Pred. No. 6.2e-142;		
Matches 733; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1;

[illegible]

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Db	437	GGGTACAAAGCTTATAGTGGCTGCGGATAGCTCTACCGGAAAGGCTCGACGGAAGAC	496
OY	487	AGTACCAAGCAGTGGGGGCGGAGCCACCAACCCAAAGATGCGGAAGCTCTTCAGTT	546
Db	497	AGTACCAAGCAGTGGGGGCGGAGCCACCAACCCAAAGATGCGGAAGCTCTTCAGTT	556
OY	547	TCACACGAGCCTGGAATCGGACCTGCAGAAGACTTCTCTCCAGGCGCTTAAGGAGTCC	606
Db	557	TCACACGAGCCTGGAATCGGACCTGCAGAAGACTTCTCTCCAGGCGCTTAAGGAGTCC	616
OY	607	AGTCTACTCGTGGAGGACCTGGAGCGGAGCTGAGGCTCTTCCAGCAACATCCGT	666
Db	617	AGTCTACTCGTGGAGGACCTGGAGCGGAGGCTGAGGCTCTTCCAGCAACATCCGT	676
OY	667	CAGCCCTGGCAATCCACCAATATATCT -GAACTGATCTTTTATACAAATATAG	725
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OY	726	AAAAGCAGCTTGAA	740
Db	737	AAAAGCAGCTTGAA	751

RESULT 4					
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DEFINITION	5', mRNA sequence.	792 bp	mRNA	linear	EST-20-FEB-2007
ACCESSION	AGNCOURT_6544142	NIH_MGC_118	Homo sapiens	CDNA clone	IMAGE:574574
VERSION	BM549665				
KEYWORDS	BM549665.1	GI:18785261			
SOURCE	EST.				
ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 792)				
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM12769 row: C column: 22
High quality sequence stop: 570.

FEATURES

Location/Qualifiers
1..792

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/clone_image="5745741"
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6, site_1: NotI, site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
BASE COUNT 182 a 241 c 242 g 122 t 5 others
ORIGIN

Query Match 97.5%; Score 721.2; DB 13; Length 792;
Best Local Similarity 98.8%; Pred. No. 9.2e-142;
Matches 726; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 6 CCGGCTGCACGGGGGTGACGGCGGAGCGGGGGTCTGTGAGCCATGCGCGCG 65
DB 19 CCGGATGCACGGGGGTGACGGCGGAGCGGGGGTCTGTGAGCCATGCGCGCG 78
OY 66 CCGGCGCCATCTGTGATGCGGTGAGAACCTGACCGCGGAGAGCTCAAGATTCAAG 125
DB 79 CCGGAGCGCCATCTGTGATGCGGTGAGAACCTGACCGCGGAGAGCTCAAGATTCAAG 138
OY 126 CTGAAGCTGCTGTGCTGCGTGGCGAGGAGGCTACGGGCGCATCCGGGCGCGCTG 185
DB 139 CTGAAGCTGCTGTGCTGCGTGGCGAGGAGGCTACGGGCGCATCCGGGCGCGCTG 198
Y 186 CTGTCCATGAGACCTTGGACTCAACGCAAGGTGTCACCTTCTACCTGAGAGACTAG 245
DB 199 CTGTCCATGAGACCTTGGACTCAACGCAAGGTGTCACCTTCTACCTGAGAGACTAG 258
OY 246 GGGCGCGAGCTACCGCTTAAGCTGCTGGCGGACATGAGGCGCTGCGAGAGATGCGGCGAG 305
DB 259 GGGCGCGAGCTACCGCTTAAGCTGCTGGCGGACATGAGGCGCTGCGAGAGATGCGGCGAG 318
OY 306 CTGCAAGCGGCAACGACGAGGCTGTGAGCGCGGCGAGCTGGGATTCAGAGCCCTCT 365
DB 319 CTGCAAGCGGCAACGACGAGGCTGTGAGCGCGGCGAGCTGGGATTCAGAGCCCTCT 378
OY 366 CAGTGGGAGCAAGGAGCGCTGACCTTATAGACGACGACGCGCTGGCTTATCGCG 425
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OY 426 AGGGTCACAAGGTTGAGTGTGCTGATGCTGTGTCGAGGAGAGTCTGACGAGTAG 485
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DB 559 TTACACGAGCTGGAACCTGGAACCTGGAAGAGTCTGCTCCAGGCGCTTAAGGAGTCC 618
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DB 619 CAGTCCACTGCTGTGAGAGACTGAGAGGAGAGCTGAGGCTCTCCAGGAGAGTCCGCG 678
OY 666 TCAGCCCGGAGCAATCCCAATCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 725
DB 679 TCAGCCCGGAGCAATCCCAATCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 738
OY 726 AAAAGCCAGCTTGA 740
DB 739 AAAAGCCAGCTTGA 753
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LOCUS
DEFINITION
602737190P1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:482182 5',
ACCESSION
BG764161
VERSION
BG764161.1 GI:14074814
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NIH-MGC <http://imgc.ncl.nih.gov/>
1 (bases 1 to 750)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCT/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLM1722 row: d column: 23
High quality sequence stop: 721.
Location/Qualifiers
1..750
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/clone_lib="NIH_MGC_49"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pORF; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 165 a 232 c 235 g 118 t
ORIGIN
Query Match 96.4%; Score 713.4; DB 12; Length 750;
Best Local Similarity 99.7%; Pred. No. 4e-140;
Matches 725; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 135 CTTGTGCTGCGCTGGAGGGCTACGGGCGCATCCGCGGGCGCGCTGCTGTCAG 194
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 Db 122 CTGTGGTCCCTGGCGAGGGCTACGGGCGCATCCGCGGGCGCGCTGCTGTCAG 181
 QY 195 GACGCTTGGACCTACCGACAGCTGTACCTTCTACCTGAGACCTACGCGCGGAG 254
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 Db 182 GACGCTTGGACCTACCGACAGCTGTACCTTCTACCTGAGACCTACGCGCGGAG 241
 QY 255 CTACCCGCTAACGCTGCGGACATGGGCTGACAGAGATGGCGGCGAGCTGACAGCG 314
 |||||||
 Db 242 CTCACCGCTAACGCTGCGGACATGGGCTGACAGAGATGGCGGCGAGCTGACAGCG 301
 QY 315 GCCAGCACAGGGCTGCGGAGCGCGGAGTGGGATCCAGGCGCTCTCCAGTCGGA 374
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 Db 302 GCCAGCACAGGGCTGCGGAGCGCGGAGTGGGATCCAGGCGCTCTCCAGTCGGA 361
 QY 375 GCCAAGCCAGGCGCTGCTTATAGACGACGCGGCTGCGCTTATCGGAGGTCACA 434
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 Db 362 GCCAAGCCAGGCGCTGCTTATAGACGACGCGGCTGCGCTTATCGGAGGTCACA 421
 Y 435 AACGTTGAGTGGCTGCTGATGCTGTACGGGAGGCTCTACGAGATGACAGTACAG 494
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 QY 495 GCAGTGGCGGCGGAGCGCCACCAACCAAGCAAGATGGGAGCTCTTCACTTCAACACA 554
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 Db 482 GCAGTGGCGGCGGAGCGCCACCAACCAAGCAAGATGGGAGCTCTTCACTTCAACACA 541
 QY 555 GCCTGGAACCTGAGCTGCAAGAGCTGCTCTCAGAGCGCCCTTAAGGAGTCCGACGTC 614
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 Db 542 GCCTGGAACCTGAGCTGCAAGAGCTGCTCTCAGAGCGCCCTTAAGGAGTCCGACGTC 601
 QY 615 CTGTGAGAGAGCTGAGAGGAGCTGAGGCTCTTCCAGCAACTCCGGTCAAGCCCT 674
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 Db 602 CTGTGAGAGAGCTGAGAGGAGCTGAGGCTCTTCCAGCAACTCCGGTCAAGCCCT 661
 QY 675 GGCAATCCCAACCAATCATCTGATCTGATCTTTTATATACA-CAATATACGAAAAACA 733
 |||||||
 Db 662 GGCAATCCCAACCAATCATCTGATCTGATCTTTTATATACGCAATATACGAAAAACA 721
 QY 734 GCTTGAA 740
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 Db 722 GCTTGA 728
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 ACCESSION B6767422
 VERSION B6767422.1 GI:14078075
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 856)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM1745 row: e column: 05
 High quality sequence stop: 696.

FEATURES
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 Location/Qualifiers
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site_1: xhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

BASE COUNT 194 a 234 c 279 g 149 t
 ORIGIN

Query Match 93.4%; Score 690.8; DB 12; Length 856;
 Best Local Similarity 99.6%; Pred. No. 2,3e-135;
 Matches 703; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 Db 2 GCGGGGTGAGCGCGGACGCGCGGAGTCTGAGGACATGGGCGCGCGGCGGCGG 61
 QY 75 ATCTGATGCGCTGAGAACTGACCGCGGAGAGCTCAAGTCAAGCTGAAGCTG 134
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 Db 62 ATCTGATGCGCTGAGAACTGACCGCGGAGAGCTCAAGTCAAGCTGAAGCTG 121
 QY 135 CTTGTGCTGCGCTGGAGGGCTACGGGCGCATCCGCGGGCGCGCTGCTGTCAG 194
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 Db 122 CTGTGGTCCCTGGCGAGGGCTACGGGCGCATCCGCGGGCGCGCTGCTGTCAG 181
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 Db 182 GACGCTTGGACCTACCGACAGCTGTACCTTCTACCTGAGACCTACGCGCGGAG 241
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 Db 242 CTCACCGCTAACGCTGCGGACATGGGCTGACAGAGATGGCGGCGAGCTGACAGCG 301
 QY 315 GCCAGCACAGGGCTGCGGAGCGCGGAGTGGGATCCAGGCGCTCTCCAGTCGGA 374
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 Db 302 GCCAGCACAGGGCTGCGGAGCGCGGAGTGGGATCCAGGCGCTCTCCAGTCGGA 361
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 Db 362 GCCAAGCCAGGCGCTGCTTATAGACGACGCGGCTGCGCTTATCGGAGGTCACA 421
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 Db 602 CTGTGAGAGAGCTGAGAGGAGCTGAGGCTCTTCCAGCAACTCCGGTCAAGCCCT 661
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 Db 662 GGCATATCCCAACCAATCATCTGATCTGATCTTTTATATACA 707

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Query Match 90.6%; Score 670.4; DB 9; Length 678;
 Best Local Similarity 99.9%; Pred. No. 4.3e-131;
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 DB TACGAGGAGTGGGCGGCGGAGCCACCAACCAAGAGTGGGAGAGCTTCTTCAAGTTTC 199
 258 TACGAGGAGTGGGCGGCGGAGCCACCAACCAAGAGTGGGAGAGCTTCTTCAAGTTTC 199
 549 ACAACGAGCTGGAATGGAGCTGCAAGAGCTTCTTCAAGAGGCTTCAAGAGGCTTCCAG 608
 DB ACAACGAGCTGGAATGGAGCTGCAAGAGCTTCTTCAAGAGGCTTCTTCAAGAGGCTTCCAG 139
 198 ACAACGAGCTGGAATGGAGCTGCAAGAGCTTCTTCAAGAGGCTTCTTCAAGAGGCTTCCAG 139
 609 TCCCTACTGCTGAGAGACCTGAGAGCGGAGCTGAGAGCTTCTTCCAGCAACATCTCGGTCA 668
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 138 TCCCTACTGCTGAGAGACCTGAGAGCGGAGCTGAGAGCTTCTTCCAGCAACATCTCGGTCA 79
 669 GCCCCTGCAATCCACCAATATCTCTGATCTGATCTTTTATACATATATACGAA 728
 DB GCCCCTGCAATCCACCAATATCTCTGATCTGATCTTTTATACATATATATACGAA 19
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 729 AGCCAGCTTGA 740
 DB 18 AGCCAGCTTGA 7

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 741)
 AUTHORS NIH-GSAC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cygabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCMI885 row: n column: 15
 High quality sequence stop: 643.
 Location/Qualifiers
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 /note="Organ: eye; Vector: pOT7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library. I"

BASE COUNT 139 a 243 c 237 g 122 t
 ORIGIN

Query Match 90.2%; Score 667.6; DB 13; Length 741;
 Best Local Similarity 97.1%; Pred. No. 1.7e-130;
 Matches 701; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

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 141 TGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 200
 187 TGTCCATGAGAGCGCTTGGACCTACGCAAGCTGTCACCTTCTACTGAGAGCTTACG 246
 DB TGTCCATGAGAGCGCTTGGACCTACGCAAGCTGTCACCTTCTACTGAGAGCTTACG 260
 201 TGTCCATGAGAGCGCTTGGACCTACGCAAGCTGTCACCTTCTACTGAGAGCTTACG 260
 247 GCGCGGAGCTCACCGCTTAACGCTGCTGCGGACATGGGCTTGCAGAGATGGCGGGGAGC 306
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 261 GCGCGGAGCTCACCGCTTAACGCTGCTGCGGACATGGGCTTGCAGAGATGGCGGGGAGC 320
 307 TGCAGGCGGCGACGACACGAGGCTCTGGAGCGGCGGACGCTGGGATCCAGGCGCTTCTC 366
 DB TGCAGGCGGCGACGACACGAGGCTCTGGAGCGGCGGACGCTGGGATCCAGGCGCTTCTC 380
 321 TGCAGGCGGCGACGACACGAGGCTCTGGAGCGGCGGACGCTGGGATCCAGGCGCTTCTC 380
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 DB AGTGGGAGCGCAAGCGGCGCTGACTTATAGACGAGCGGCGCTTATTCGCGA 440
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 441 GGGTCACAAACGTTGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 500
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 DB TCACACGAGCGCTGGAAGCTGCAAGAGCTTCTCTCAAGGCGCTTAAGGAGTCCC 620

Mon Dec 16 07:22:19 2002

us-09-728-721-48.1.st

Page 8

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QY 607 AGTCTTACCTGATGAGGAGCT-6GAGCGGAGCGAGGCTCTTCCACAGACACTCGG 665
DB 621 AGTCTTACCTGATGAGGAGCTGAGGAGCTCTTCCACAGACACTCGG 680
QY 666 TCAGCCCTGCGCATCCACCAATCATCTGATCTTTATACACATATACG 725
DB 681 TCAGCCCTGCGCAT-CCACCAATCATCTGATCTTTATACACATATACG 739
QY 726 AA 727
DB 740 AA 741

RESULT 10
LOCUS BM972785 676 bp mRNA linear EST 21-MAR-2002
DEFINITION UI-CF-ECL-abr-k-24-0-UI.s1 UI-CF-ECL Homo sapiens cDNA clone
VERSION BM972785
KEYWORDS BM972785.1 GI:19590376
SOURCE EST.
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 676)
JOURNAL Normalization and subtraction: two approaches to facilitate gene
COMMENT discovery
genome Res. 6 (9), 791-806 (1996)
97044477
McCrack Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccrack@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
Location/Qualifiers
1..676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-ECL-abr-k-24-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a
modified polylinker; Site: 1: EcoR 1; Site 2: Not I;
UI-CF-ECL is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTCTTAC.
TAG_LIB=UI-CF-ECL
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371

BASE COUNT 112 a and 380-383
TAG_SEQ=AAAGTCTTAC"
ORIGIN 199 c 211 g 154 t
Query Match 89.2%; Score 660; DB 14; Length 676;
Best Local Similarity 100.0%; Pred. No. 6.6e-129;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GATGCGCTGAGAACCTGACCGCGGAGAGCTCAAGAGTTCAAGCTGCTGCG 140
DB 676 GATGCGCTGAGAACCTGACCGCGGAGAGCTCAAGAGTTCAAGCTGCTGCG 617
QY 141 GTGCCGCTGCGGAGGCTGACGGGCGATCCCGGGGGCGGCTGCTGCTGAC 200
DB 616 GTGCCGCTGCGGAGGCTGACGGGCGATCCCGGGGGCGGCTGCTGCTGAC 557
QY 201 TTGAGACCTACCGACCAAGCTGTCAGCTTACCTGAGAGACCTAGCGCGG 260
DB 556 TTGAGACCTACCGACCAAGCTGTCAGCTTACCTGAGAGACCTAGCGCGG 497
QY 261 GCTAACGTCGTCGCGGACATGAGGCTGACGAGATGAGCGGAGCTGACGCG 320
DB 496 GCTAACGTCGTCGCGGACATGAGGCTGACGAGATGAGCGGAGCTGACGCG 437
QY 321 CACCAAGGCTGAGAGCGCGCCAGCTGAGATCAGGCGCTCTTATGTCGACG 380
DB 436 CACCAAGGCTGAGAGCGCGCCAGCTGAGATCAGGCGCTCTTATGTCGACG 377
QY 381 CCAGGCTGCTGATTTATGACCAAGACAGCGGCGGCTTATGCGAGGTCAC 440
DB 376 CCAGGCTGCTGATTTATGACCAAGACAGCGGCGGCTTATGCGAGGTCAC 317
QY 441 GAGTGGCTGCTGATTTATGACCAAGACAGCGGCGGCTTATGCGAGGTCAC 500
DB 316 GAGTGGCTGCTGATTTATGACCAAGACAGCGGCGGCTTATGCGAGGTCAC 257
QY 501 CGAGCGGACCGCCACCAACCAAGCAAGTGGAGAGTCTTCAAGTTTCAACAG 560
DB 256 CGAGCGGACCGCCACCAACCAAGCAAGTGGAGAGTCTTCAAGTTTCAACAG 197
QY 561 AACTGACCTGCAAGAGCTGCTGCTGAGGCGCTTACAGGAGTCCAGTCTG 620
DB 196 AACTGACCTGCAAGAGCTGCTGCTGAGGCGCTTACAGGAGTCCAGTCTG 137
QY 621 GAGGACCTGAGAGCGGAGGCTGAGGCTGCTGAGGAGTCCAGTCTGAGG 680
DB 136 GAGGACCTGAGAGCGGAGGCTGAGGCTGCTGAGGAGTCCAGTCTGAGG 77
QY 681 CCCACCAATCATCTGATCTTTATACAAATATGAAAGCCAGCTTGA 740
DB 76 CCCACCAATCATCTGATCTTTATACAAATATGAAAGCCAGCTTGA 17

RESULT 11
BE908204 675 bp mRNA linear EST 20-OCT-2000
LOCUS 601500461p1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902319 5',
DEFINITION RNA sequence.
ACCESSION BE908204
VERSION BE908204.1 GI:10402543
KEYWORDS EST.
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH_MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: ATCC
```

cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9704 row: j column: 16
High quality sequence stop: 660.

FEATURES

source

1..675

Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3902319"
/clone.lib="NIH_MGC_70"
/tissue_type="epithelial carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: PCMV-SPORT6; Site:1; NotI;
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

BASE COUNT 151 a 214 c 198 g 112 t
ORIGIN

Query Match

Best Local Similarity 99.5%; Score 654.2; DB 12; Length 675;

Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FEATURES

source

1..744

Location/Qualifiers

cdna Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM10302 row: m column: 17
High quality sequence stop: 661.

FEATURES

source

1..744

Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4476088"
/clone.lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: PCMV-SPORT6; Site:1; NotI;
Site:2; SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 159 a 227 c 238 g 120 t
ORIGIN

Query Match

Best Local Similarity 97.0%; Score 647.4; DB 12; Length 744;

Matches 713; Conservative 0; Mismatches 16; Indels 6; Gaps 5;

QY 82 ATGCGCTGAGAACTGACCGCCGAGAGCTCAAGATTCAAGTCAAGCTGCTCGG 141
DB 1 ATGCGCTGAGAACTGACCGCCGAGAGCTCAAGATTCAAGTCAAGCTGCTCGG 60
QY 142 TGGCGCTGCGGCGGCTACGGCGGCGATCCCGGGGGCGCGCTGCTCATGAGAGCT 201
DB 61 TGGCGCTGCGGCGGCTACGGCGGCGATCCCGGGGGCGCGCTGCTCATGAGAGCT 120
QY 202 TGGAGCTCAACGACAGCTGCTGACCTTCTACCTGAGAGCTACGGCGCGAGCTCACC 261
DB 121 TGGAGCTCAACGACAGCTGCTGACCTTCTACCTGAGAGCTACGGCGCGAGCTCACC 180
QY 262 CTACAGCTGCTGCGGCGATGCGGCTGCGAGAGATGCGCGGGCGAGCTGCAAGCGCGCACGC 321
DB 181 CTACAGCTGCTGCGGCGATGCGGCTGCGAGAGATGCGCGGGCGAGCTGCAAGCGCGCACGC 240
QY 322 ACCAGGCGCTGAGCGCGCGCGAGCTGGAGTCCAGGCGCTCTCTCATGTCGGCGCAAGC 381
DB 241 ACCAGGCGCTGAGCGCGCGAGCTGGAGTCCAGGCGCTCTCTCATGTCGGCGCAAGC 300
QY 382 CAGGCGCTGACTTTATAGACACAGCAGCGGCTGCTTATCGGAGGGTCAAAAGCTTG 441
DB 301 CAGGCGCTGACTTTATAGACACAGCAGCGGCTGCTTATCGGAGGGTCAAAAGCTTG 360
QY 442 AGTGGCTGCTGATGCTGCTGTACGAGGAGTCTGACGGATGAGCAGTACAGGAGTGC 501
DB 361 AGTGGCTGCTGATGCTGCTGTACGAGGAGTCTGACGGATGAGCAGTACAGGAGTGC 420
QY 502 GGGCGGAGCGCCCAACCAAGCAAGATGCGGAGCTCTTCACTTCAACACAGCGCTTGA 561
DB 421 GGGCGGAGCGCCCAACCAAGCAAGATGCGGAGCTCTTCACTTCAACACAGCGCTTGA 480
QY 562 ACTGAGCTGCAAGAGCTGCTCTTCAGAGCGCTTAAAGGAGTCCAGTCTTCACTGTTG 621
DB 481 ACTGAGCTGCAAGAGCTGCTCTTCAGAGCGCTTAAAGGAGTCCAGTCTTCACTGTTG 540
QY 622 AGGAGCTGAGAGGAGCTAGGCTCTTCCAGCAACACTCGGTCAGGCGCTGAGCAATC 681
DB 541 AGGAGCTGAGAGGAGCTAGGCTCTTCCAGCAACACTCGGTCAGGCGCTGAGCAATC 600
QY 682 CCACCAATCATCTGATCTGATCTTTTATACAAATATAGAAAGCAGCTTGAA 740
DB 601 CCACCAATCATCTGATCTGATCTTTTATACAAATATAGAAAGCAGCTTGAA 655

RESULT 12

RG255521
LOCUS RG255521 744 bp mRNA linear EST 13-FEB-2001
DEFINITION B02367671P1 NIH_MGC_91 Homo sapiens cdna clone IMAGE:4476088 5',
mRNA sequence.
ACCESSION RG255521
VERSION BG255521.1 GI:12765259
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 744)
NIH-MGC <http://imgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
COMMENT cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM10302 row: m column: 17
High quality sequence stop: 661.

QY 8 GCGTCGAGCGGAGTGAGCGCGGCGAGCGCGGAGTCTGAGAGCATGGCGCGCGCG 67
DB 1 GCGTCGAGCGGAGTGAGCGCGGCGAGCGCGGAGTCTGAGAGCATGGCGCGCGCG 60
QY 68 CGAGCGCATCTGATGCGCTGAGAGACCTGACCGCGGAGAGCTCAAGATTCAAGCT 127
DB 61 CGAGCGCATCTGATGCGCTGAGAGACCTGACCGCGGAGAGCTCAAGATTCAAGCT 120
QY 128 GAAGCTGCTGCTGCTGCGGCGGAGGCTACGGGCGGAGTCCCGGGCGCGCGTGT 187
DB 121 GAAGCTGCTGCTGCTGCGGCGGAGGCTACGGGCGGAGTCCCGGGCGCGCGTGT 180
QY 188 GTCCATGAGAGCGCTTGGAGCTACCGCAAGAGTGTGACCTTCTTACCTGGAGACTTAC 247
DB 181 GTCCATGAGAGCGCTTGGAGCTACCGCAAGAGTGTGACCTTCTTACCTGGAGACTTAC 240
QY 248 CGCGGAGTCAACCGCTTACGCTGCGGAGCATGGGCTGCGAGAGATGGCGGCGAGCT 307
DB 241 CGCGGAGTCAACCGCTTACGCTGCGGAGCATGGGCTGCGAGAGATGGCGGCGAGCT 300
QY 308 GCGAGGCGGCGAGCAACAGGCTGAGGCGGCGGAGCTGGGAGTCCAGGCGCGCTCTCA 367
DB 301 GCGAGGCGGCGAGCAACAGGCTGAGGCGGCGGAGCTGGGAGTCCAGGCGCGCTCTCA 360
QY 368 GTGCGGAGCGCAAGCGAGCGCTGACTTTATAGACGACACCGGCGTGCCTTATCCGAG 427
DB 361 GTGCGGAGCGCAAGCGAGCGCTGACTTTATAGACGACACCGGCGTGCCTTATCCGAG 420

QY	428	GGTCACAAAGCTGATGGCTCTGGATGCTCTGTACGGGAAGTCTGTACGGATAGCA	487
Db	421	GGTCACAAAGCTGATGGCTCTGGATGCTCTGTACGGGAAGTCTGTACGGATAGCA	480
QY	488	GTACCAAGCAGTGGGGCCGAGACCCCAACCCAAAGCAAGATGGGAAGCTCTTCAGTTT	547
Db	481	GTACCAAGCAGTGGGGCCGAGACCCA -CAACCCAAAGCAAGATGGGAAGCTCTTCAGTTT	539
QY	548	CACACACAGCTGGAACTGTGACTGCAAGAGACTGTCTCTCCAGGCCCTTAAGGAGTCCCA	607
Db	540	CACACACAGCT -GAACTGTGACTGCAAGAGACTGTCTCTCCAGG -CCTTAAGGAGATGCCA	597
QY	608	GTCCTACCTGATGATGAGACCTGAGACGGAGCTGAGCTCCCTCCACCAATACGGTCC	667
Db	598	GTCCTACCTGATGATGAGACCTGAGACGGAGCTGAGGCT -CTTCCAGGCACAACTCCGGTCC	656
QY	668	AGGCCCTGGCAATCCCAACAATCATCTCCGAAAT - -CTGATCTCTTTTATACAAATATACG	725
Db	657	AGGCCCTGGCAATCCCAACAATCATCTGATCTGATCTTTTATACAAATATACG	716
QY	726	AAAAGCCAGCTTGAA	740
Db	717	AAAAGCCAGCTTGAA	731

RESULT 13	
BE909218	
LOCUS	
DEFINITION	687 bp mRNA linear EST 20-OCT-2000
ACCESSION	B01501478F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903498 5'
VERSION	mRNA sequence.
FEATURES	BE909218
	BE909218.1 GI:10404770

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euteleia; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 687)
 NIH-MGC <http://mgc.ncl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC).
 Unpublished (1999)
 Contact: Robert Strausberg Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The M.A.G.E. Consortium (LNL1)
DNA Sequencing by: The MAGE Genomics, Inc.
Source: MAGE Genomics, Inc. Clone distribution information can be found through the M.A.G.E. Consortium/LNL1 at: <http://image.lnl1.gov>
Plate: L1M9707 row: k column: 19
High quality sequence stop: 673
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:3903498
/clone_1id="NTH.MGC.70"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Pancreas; Vector: PCMV-SPOrt6; Site1: NotI; Site2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.1 kb. Library constructed by Life Technologies."

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Query Match	86.4%	Score 639	DB 12	Length 687
Best local Similarity	98.7%	Pred. No. 1,78	124	
Matches 676	Conservative 0	Mismatches 5	Indels 4	Gaps 3
48	GGAGCCATGGGGCGCCG-CGCGGACGCCATCCTGGATCGCTGGAGGAACTGACCGCCGA	106		

Db	1	GGAGCCCTGGGGGCGCCGGCGGACGCCATCCTGGATGCGCTGGAGAACTGTGACCGCGGA	60
QY	107	GGAGGCTCAGAAATTCCTCAAGCTCAAGCTGCTGTGCGGTGGCGGTGCGCAAGGGCTACGGGGG	166
Db	61	GGAGGCTCAGAAATTCCTCAAGCTCAAGCTGCTGTGCGGTGGCGGTGCGCAAGGGCTACGGGGG	120
QY	167	CATCCCGCGGGGCGGCGCTGCTGTCCATGAGACCCCTTGAGACTTCACCAACAAGTGTGTAG	226
Db	121	CATCCCGCGGGGCGGCGCTGCTGTCCATGAGACCCCTTGAGACTTCACCAACAAGTGTGTAG	180
QY	227	CTTCTACCTGAGAACCTACGGGCGCGAGCTCACCGCTAACGTGTGCGCAACTGGGCGCT	286
Db	181	CTTCTACCTGAGAACCTACGGGCGCGAGCTCACCGCTAACGTGTGCGCAACTGGGCGCT	240
QY	287	GCAGGAGATGGCGGGGACACTGCAGGCGGGCCACGACACAGAGGCTCTTGAGACCCCGGCAC	346
Db	241	GCAGGAGATGGCGGGGACACTGCAGGCGGGCCACGACACAGAGGCTCTTGAGACCCCGGCAC	300
QY	347	TGGGATCCAGGGCCCTCTCTCAAGTGGGACCAAGCCAGGCGCTGCACCTTATTAGACGACA	406
Db	301	TGGGATCCAGGGCCCTCTCTCAAGTGGGACCAAGCCAGGCGCTGCACCTTATTAGACGACA	360
QY	407	CCGGGCTGGCGTTATCGCGAGGGGTCAACAAAGCTTGAGTGGCTGCTGGATCTCTGTACGG	466
Db	361	CCGGGCTGGCGTTATCGCGAGGGGTCAACAAAGCTTGAGTGGCTGCTGGATCTCTGTACGG	420
QY	467	GAAGGTCCTGACGATGAGACAGTACCAGGCAAGTGGGGCGCGAGCCACCAACCCAAAGCAA	526
Db	421	GAAGGTCCTGACGATGAGACAGTACCAGGCAAGTGGGGCGCGAGCCACCAACCCAAAGCAA	480
QY	527	GATGCGGAAGCTTCTCAGTTTCACACGACGCTTGAAGACTGACGCTGCAAGAGACTTGGCTCT	586
Db	481	GATGCGGAAGCTTCTCAGTTTCACACGACGCTTGAAGACTGACGCTGCAAGAGACTTGGCTCT	540
QY	587	CCAGGCCCTTAAGGAGTCCCAAGTCTTACCTGATGAGAGACCTTGAGCGGAGCTGAGGCTC	646
Db	541	CCAGGCCCTTAAGGAGTCCCAAGTCTTACCTGATGAGAGACCTTGAGCGGAGCTGAGGCTC	600
QY	647	CTTCCCGACCAACTCCGGTCAAGCCCTGGCAATCCACCAAAATCATCTGAAATCTGATC	706
Db	601	-TTCCCGACCAACTCCGGTCAAGCCCTGGG--AATCCCAACCAATCATCTGAAATCTGATC	657
QY	707	TTTTTATTACCAATATTAGAAAAAGC 731	
Db	658	TTTTTATTACCAATATTAGAAAAAGC 682	

RESULT 14	
BM98354/c	
LOCUS	
DEFINITION	BM98354 638 bp mRNA linear EST 17-JUN-2002
ACCESSION	U1-HIT1-awc-p-21-0-U1.s1 NC1_CGAP-DT1 Homo sapiens
VERSIONS	IMAGE:5887748 3, mRNA sequence.
KEYWORDS	BM98354
SOURCE	BM98354.1 GI:19732355
ORGANISM	human
REFERENCE	Eukaryotes Homo sapiens
AUTHORS	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
TITLE	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
JOURNAL	1 (bases 1 to 638)
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
	Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-rt@mail.nih.gov
	Tissue Procurement: Dr. Jose Mercuende
	cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
	Clone Distribution: Clone distribution information can be found
	through the I.M.A.G.E. Consortium/HLN at: http://image.lln.gov

Seq primer: M13 FORWARD
POLA+yes.

FEATURES
Location/Qualifiers

1..638
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:5887748"
/clone_lib="NCI_CGAP_DTL1"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_DTL1 is a normalized cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in lung. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTCGG.
TAG_LIB=UI-H-DT1
TAG_TISSUE=Lung metastatic chondrosarcoma
TAG_SEQ=AACTGTCGG"
BASE COUNT 108 a 185 c 201 g 144 t
ORIGIN

Query Match

Best Local Similarity 99.5%; Pred. No. 6.6e-120;
Matches 619; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 119 GTTCAAGCTGAAGCTGCTGCTGCGGCGAGGCTACGGGCGATCCCGGGG 178
DB 638 GTCAAGCTGAAGCTGCTGCTGCGGCGAGGCTACGGGCGATCCCGGGG 579
QY 179 CGCGCTGCTGCATGAGAGCGCTTGACCTCAACCGCAAGCTGTGACTTCTACTGA 238
DB 578 CGCGCTGCTGCATGAGAGCGCTTGACCTCAACCGCAAGCTGTGACTTCTACTGA 519
QY 239 GACTTACGCGCGGAGCTACCGCTTACCTGTCGCGCATGAGGCTCGAGAGATGGC 298
DB 518 GACTTACGCGCGGAGCTACCGCTTACCTGTCGCGCATGAGGCTCGAGAGATGGC 459
QY 299 CGGCGAGCTGCAAGCGCGGCGACGACGAGGCTGTGAGCGCGGCGAGCTGGATCCAGGC 358
DB 458 CTGGCGAGCTGCAAGCGCGGCGACGACGAGGCTGTGAGCGCGGCGAGCTGGATCCAGGC 399
QY 359 CCCTCTCTAGTGGGCGGCGCAAGCGGCTGACCTTATAGACACAGCGGCTCGCT 418
DB 398 CCCTCTCTAGTGGGCGGCGCAAGCGGCTGACCTTATAGACACAGCGGCTCGCT 339
QY 419 TATCGGAGGCTCACAAAGTGTGAGTGTGCTGATGCTGTAGCGGAAGTCTGTAC 478
DB 338 TATCGGAGGCTCACAAAGTGTGAGTGTGCTGATGCTGTAGCGGAAGTCTGTAC 279
QY 479 GGATGAGAGTACCAAGGAGTGGGCGGCGACGCGCAACCAAGCAAGATGCGAAGCT 538
DB 278 GGATGAGAGTACCAAGGAGTGGGCGGCGACGCGCAACCAAGCAAGATGCGAAGCT 219
QY 539 CTTCAGTTTACACACAGCTGAGACTGACCTGCAAGGACTGTCTCTCCAGGCTTAAG 598
DB 218 CTTCAGTTTACACACAGCTGAGACTGACCTGCAAGGACTGTCTCTCCAGGCTTAAG 159
QY 599 GGAGTCCAGTCTACTGCTGTGAGAGACTGAGAGGAGCTGAGGCTCTCTCCACCAAC 658
DB 158 GGAGTCCAGTCTACTGCTGTGAGAGACTGAGAGGAGCTGAGGCTCTCTCCACCAAC 99
QY 659 ACTCGGTCAGCCCTGGCAATCCCAACAATCATCTGAATCTGATCTTTTATACACA 718
|||||

DB 98 ACTCGGTCAGCCCTGGCAATCCCAACAATCATCTGAATCTGATCTTTTATACACA 39

QY 719 ATATACGAAAGCCAGCTTGAA 740
DB 38 ATATACGAAAGCCAGCTTGAA 17

RESULT 15

BM456838

LOCUS BM456838 1079 bp mRNA linear EST 05-FEB-2002

DEFINITION AGENCOURT_6404153 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583760

5', mRNA sequence.

ACCESSION BM456838

VERSION BM456838.1 GI:18505878

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at:

<http://image.llnl.gov>

Plate: LHM12347 row: f column: 17

High quality sequence stop: 682.

FEATURES

source

location/Qualifiers

1..1079

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:5583760"

/clone_lib="NIH_MGC_92"

/tissue_type="Embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: testis; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 246 a 360 c 297 g 171 t

ORIGIN

Query Match

Best Local Similarity 92.2%; Pred. No. 2.2e-118;
Matches 677; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

QY 7 CGGCTGACGCGGGGTGAGCGGCGGCGGCGGAGTCTTGAGGCGGCGGCGGCGG 66
DB 16 CGGCTGACGCGGGGTGAGCGGCGGCGGCGGCGGAGTCTTGAGGCGGCGGCGG 75
QY 67 GCGAGCCATCTGTGATGCGCTGAGAGACCTGACCGCGAGAGAGCTCAAGATTCAAC 126
DB 76 GCGAGCCATCTGTGATGCGCTGAGAGACCTGACCGCGAGAGAGCTCAAGATTCAAC 135
QY 127 TGAAGTGTGTGGTGGCGGCGGCGGAGGCGTACGCGGCGGCGGCGGCGGCGCTGC 186
DB 136 TGAAGTGTGTGGTGGCGGCGGCGGAGGCGTACGCGGCGGCGGCGGCGGCGCTGC 195
QY 187 TGTTCATGAGCGCTTGAGACTTACCGAGACGCTGCTACCTGAGAGACTTACG 246
DB 196 TGTTCATGAGCGCTTGAGACTTACCGAGACGCTGCTACCTGAGAGACTTACG 255
QY 247 GCGCGAGGCTCAACCGCTTAACGCTGCGGAGACATGAGGCGCTGACAGAGATGGCGGCGACG 306
DB 256 GCGCGAGGCTCAACCGCTTAACGCTGCGGAGACATGAGGCGCTGACAGAGATGGCGGCGACG 315
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Mon Dec 16 07:22:19 2002

us-09-728-721-48.rst

Page 12

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OY 307 TGCAGGCGGCCACGACCGAGGGCTCTGAGCCGCCAGCTGGGATCCAGGCCCTCCTC 366
    |||||||
Db 316 TGCAGGCGGCCACGACCGAGGGCTCTGAGCCGCCAGCTGGGATCCAGGCCCTCCTC 335
    |||||||
OY 367 AGTCGGCAGCCAGGCGCTGACCTTTATAGACGACGCGGCTGGCTTATCGCA 426
    |||||||
Db 336 -----GGCTGCACTTTATAGACGACGCGGCTGGCTTATCGCA 378
    |||||||
OY 427 GGGTCAAAAGCTTGTAGTGGCTGCTGATGCTGTACGGAGGTCTGACGATGAGC 486
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Db 379 GGGTCAAAAGCTTGTAGTGGCTGCTGATGCTGTACGGAGGTCTGACGATGAGC 438
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OY 487 AGTACCAGGAGTGGGCGGCGGAGCCACCAACCCAGCAAGATCGGAGCTTTCAGTT 546
    |||||||
Db 439 AGTACCAGGAGTGGGCGGCGGAGCCACCAACCCAGCAAGATCGGAGCTTTCAGTT 498
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OY 547 TCACACAGGCTGGAACCTGAGCTGCAAGGACTTGTCTCCAGGCCCTAAGGAGTCCC 606
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Db 499 TCACACAGGCTGGAACCTGAGCTGCAAGGACTTGTCTCCAGGCCCTAAGGAGTCCC 558
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OY 607 AGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCTTCCAGCACTCCGCT 666
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Db 559 AGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCTTCCAGCACTCCGCT 618
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OY 667 CAGCCCTGGCAATCCCAACCAATCATCTGAAATCTGATCTTTTATACAAATATACGA 726
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Db 619 CAGCCCTGGCAATCCCAACCAATCATCTGAAATCTGATCTTTTATACAAATATACGA 678
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OY 727 AAAGCCAGCTTGAA 740
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Db 679 AAAGCCAGCTTGAA 692
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Search completed: December 13, 2002, 09:48:55
Job time : 2175 secs

D	b		121	TCAAGCTGAACGTGCTGTGTGGTCCCGCTGCCGCAGAGGCTACTACGGCGCATTCCTCCGGGGC	180
O	y		181	CGCCTGCTGCATAGAACGCTTTGGAACTCACACCAAGCTGGTCACTTCTTAAGTGAGA	240
D	b		181	CGCTGCTGTCTAATGAAAGCCTTTGGACCTTCAACCACAAGCTGGTCACTTCTTAAGTGAGA	240
O	y		241	CTTACGCGCCCGCAAGCTCACCCCTTAACGTGCTGGCGCAATGGGCTTCGAGAGATGGCG	300
D	b		241	CTTACGCGCGCCGCAAGCTCACCCCTTAACGTGCTGGCGCAATGGGCTTCGAGAGATGGCG	300
O	y		301	GCGAGCTGCAGGCGCGCCACGCAACGAGGGCTTGGAGCGCGCGCAGCTGGGATCCAGGCC	360
D	b		301	GCGAGCTGCAGGCGCGCCACGCAACGAGGGCTTGGAGCGCGCGCAGCTGGGATCCAGGCC	360
O	y		361	CTCTCTAGTGGGAGCCAAAGCCAGGCTTCGACTTTATAGACGACGACGGGCTCGGCTTA	420
D	b		361	CTCTCTAGTGGGAGCCAAAGCCAGGCTTCGACTTTATAGACGACGACGGGCTCGGCTTA	420
Y			421	TCGCGAGGAGGTCAAAACGTTTAGTGGCTGCTGTGATCTCTGTATGAGGAGAGGCTCTGACG	480
D	b		421	TCGCGAGGAGGTCAAAACGTTTAGTGGCTGCTGTGATCTCTGTATGAGGAGAGGCTCTGACG	480
O	y		481	ATGAGCAGTACACGACGACGAGCGGGCCGAGCCACCAACCAAGCAAGATGCGGAAAGCTCT	540
D	b		481	ATGAGCAGTACACGACGACGAGCGGGCCGAGCCACCAACCAAGCAAGATGCGGAAAGCTCT	540
O	y		541	TCAGTTTCAACACAGCTGTGAAATCTGSACTCTGCAAGGACTTGTCTCCAGGCTCTAAGG	600
D	b		541	TCAGTTTCAACACAGCTGTGAAATCTGSACTCTGCAAGGACTTGTCTCCAGGCTCTAAGG	600
O	y		601	AGTCCAGTCTTACCTGGTGGAGGAGACCTCGAAGGAGGAGCTGAGAGCTCTTCCACACAC	660
D	b		601	AGTCCAGTCTTACCTGGTGGAGGAGACCTCGAAGGAGGAGCTGAGAGCTCTTCCACACAC	660
O	y		661	TCGCGTACGCCCCCTGGCAATCCCAACCAATCATCTGAATCTGATCTTTATACAAAT	720
D	b		661	TCGCGTACGCCCCCTGGCAATCCCAACCAATCATCTGAATCTGATCTTTATACAAAT	720
O	y		721	ATACGAAAAGCCACGCTTGA	740
D	b		721	ATACGAAAAGCCACGCTTGA	740
RESULT 2					
US-09-996-617-7					
Sequence 7, Application US/09996617					
Patent No. US20020128198A1					
GENERAL INFORMATION:					
APPLICANT: Berlin, John					
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED					
FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF					
FILE REFERENCE: 07334-340001					
CURRENT APPLICATION NUMBER: US/09/996,617					
PRIORITY FILING DATE: 2001-11-27					
PRIOR APPLICATION NUMBER: 09/931,071					
PRIORITY FILING DATE: 2001-08-15					
PRIOR APPLICATION NUMBER: 09/428,252					
PRIORITY FILING DATE: 1999-10-27					
PRIOR APPLICATION NUMBER: 09/340,620					
PRIORITY FILING DATE: 1999-06-28					
NUMBER OF SEQ ID NOS: 10					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 7					
LENGTH: 740					
TYPE: DNA					
ORGANISM: Homo sapiens					
FEATURES:					
NAME/KEY: CDS					
LOCATION: (34)...(638)					
US-09-996-617-7					
Query Match					
100.0%; Score 740; DB 10; Length 740;					

[illegible]

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-996-617-10

Query Match 100.0%; Score 740; DB 10; Length 740;
Best Local Similarity 100.0%; Pred. No. 3e-172;
Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGTCCGGCTGACAGCGGGGTGAGCGCGCGACCGCGCGGATCCTGGAGCCATGCGGC 60
DB 740 CGCGTCCGGCTGACAGCGGGGTGAGCGCGCGACCGCGCGGATCCTGGAGCCATGCGGC 681
QY 61 GCGCGCGCGACCGCATCTCTGGATGCGGCTGGAGAACCTGACCGCCGAGAGCTCAAGAACT 120
DB 680 GCGCGCGCGACCGCATCTCTGGATGCGGCTGGAGAACCTGACCGCCGAGAGCTCAAGAACT 621
QY 121 TCAAGCTGAAGCTGCTGCTGGTGGCGGCTGCGGAGGGGCTACGGGCGCATCCCGCGGGGCG 180
DB 620 TCAAGCTGAAGCTGCTGCTGGTGGCGGCTGCGGAGGGGCTACGGGCGCATCCCGCGGGGCG 561
QY 181 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACGCTGCTCACTTCTACTTGAGAGA 240
DB 560 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACGCTGCTCACTTCTACTTGAGAGA 501
QY 241 CCTACGGCGCGAGCTCACCGCTTAACGTGCTGCGGACATGAGGAGCTGACAGAGATGGCG 300
DB 500 CCTACGGCGCGAGCTCACCGCTTAACGTGCTGCGGACATGAGGAGCTGACAGAGATGGCG 441
QY 301 GGCAGCTGAGCGCGGCGACACGAGGCTGAGAGCGCGCGCGAGCTGGGATCCAGAGCCG 360
DB 440 GGCAGCTGAGCGCGGCGACACGAGGCTGAGAGCGCGCGAGCTGGGATCCAGAGCCG 381
QY 361 CTCCTCAGTCGCGACGCAAGCGCTGACCTTATAGCAGCAGCGGCTGCGCTTA 420
DB 380 CTCCTCAGTCGCGACGCAAGCGCTGACCTTATAGCAGCAGCGGCTGCGCTTA 321
QY 421 TCGCGAGGGTCAACAAAGTTGAGTGGCTGCTGATGCTCTGTACGGGAAAGTCTGACGG 480
DB 320 TCGCGAGGGTCAACAAAGTTGAGTGGCTGCTGATGCTCTGTACGGGAAAGTCTGACGG 261
QY 481 ATGAGAGATACAGGAGAGTGGCGGCGAGCCAGCCACCAACCAAGCAAGATGCGGAAGCT 540
DB 260 ATGAGAGATACAGGAGAGTGGCGGCGAGCCAGCCACCAAGCAAGATGCGGAAGCT 201
QY 541 TCAGTTTTCACACAGCCTGGAAGTGGACCTGCAAGGACTTGTCTCCAGAGCCCTTAAGGG 600
DB 200 TCAGTTTTCACACAGCCTGGAAGTGGACCTGCAAGGACTTGTCTCCAGAGCCCTTAAGGG 141
QY 601 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 660
DB 140 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 81
QY 661 TCCGGTACAGCCCTGGCAATCCCAACAATCATCTGATCTGATCTTTTATACCAAT 720
DB 80 TCCGGTACAGCCCTGGCAATCCCAACAATCATCTGATCTGATCTTTTATACCAAT 21
QY 721 ATACGAAAAGCCAGCTTGAA 740
DB 20 ATACGAAAAGCCAGCTTGAA 1

RESULT 4
US-09-841-879B-4
; Sequence 4, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-330001

; CURRENT APPLICATION NUMBER: US/09/841,879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(638)
US-09-841-879B-4

Query Match 100.0%; Score 740; DB 10; Length 740;
Best Local Similarity 100.0%; Pred. No. 3e-172;
Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGTCCGGCTGACAGCGGGGTGAGCGCGCGACCGCGCGGATCCTGGAGCCATGCGGC 60
DB 1 CGCGTCCGGCTGACAGCGGGGTGAGCGCGCGACCGCGCGGATCCTGGAGCCATGCGGC 60
QY 61 GCGCGCGCGACCGCATCTCTGGATGCGGCTGGAGAACCTGACCGCCGAGAGCTCAAGAACT 120
DB 61 GCGCGCGCGACCGCATCTCTGGATGCGGCTGGAGAACCTGACCGCCGAGAGCTCAAGAACT 120
QY 121 TCAAGCTGAAGCTGCTGCTGGTGGCGGCTGCGGAGGGGCTACGGGCGCATCCCGCGGGGCG 180
DB 121 TCAAGCTGAAGCTGCTGCTGGTGGCGGCTGCGGAGGGGCTACGGGCGCATCCCGCGGGGCG 180
QY 181 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACGCTGCTCACTTCTACTTGAGAGA 240
DB 181 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACGCTGCTCACTTCTACTTGAGAGA 240
QY 241 CCTACGGCGCGAGCTCACCGCTTAACGTGCTGCGGACATGAGGAGCTGACAGAGATGGCG 300
DB 241 CCTACGGCGCGAGCTCACCGCTTAACGTGCTGCGGACATGAGGAGCTGACAGAGATGGCG 300
QY 301 GGCAGCTGAGCGCGGCGACACGAGGCTGAGAGCGCGCGAGCTGGGATCCAGAGCCG 360
DB 301 GGCAGCTGAGCGCGGCGACACGAGGCTGAGAGCGCGCGAGCTGGGATCCAGAGCCG 360
QY 361 CTCCTCAGTCGCGACGCAAGCGCTGACCTTATAGCAGCAGCGGCTGCGCTTA 420
DB 361 CTCCTCAGTCGCGACGCAAGCGCTGACCTTATAGCAGCAGCGGCTGCGCTTA 420
QY 421 TCGCGAGGGTCAACAAAGTTGAGTGGCTGCTGATGCTCTGTACGGGAAAGTCTGACGG 480
DB 421 TCGCGAGGGTCAACAAAGTTGAGTGGCTGCTGATGCTCTGTACGGGAAAGTCTGACGG 480
QY 481 ATGAGAGATACAGGAGAGTGGCGGCGAGCCAGCCACCAACCAAGCAAGATGCGGAAGCT 540
DB 481 ATGAGAGATACAGGAGAGTGGCGGCGAGCCAGCCACCAACCAAGCAAGATGCGGAAGCT 540
QY 541 TCAGTTTTCACACAGCCTGGAAGTGGACCTGCAAGGACTTGTCTCCAGAGCCCTTAAGGG 600
DB 541 TCAGTTTTCACACAGCCTGGAAGTGGACCTGCAAGGACTTGTCTCCAGAGCCCTTAAGGG 600
QY 601 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 660
DB 601 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 660
QY 661 TCCGGTACAGCCCTGGCAATCCCAACAATCATCTGATCTGATCTTTTATACCAAT 720
DB 661 TCCGGTACAGCCCTGGCAATCCCAACAATCATCTGATCTGATCTTTTATACCAAT 720
QY 721 ATACGAAAAGCCAGCTTGAA 740
DB 721 ATACGAAAAGCCAGCTTGAA 740


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RESULT 7
US-09-728-721-50
: Sequence 50, Application US/09728721
: Patent No. US20020061845A1
: GENERAL INFORMATION:
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334-12A001
: CURRENT APPLICATION NUMBER: US/09/728,721
: CURRENT FILING DATE: 2000-12-01
: PRIOR APPLICATION NUMBER: 09/340,620
: PRIOR FILING DATE: 1999-06-28
: PRIOR APPLICATION NUMBER: US 09/207,359
: PRIOR FILING DATE: 1998-12-08
: PRIOR APPLICATION NUMBER: US 09/099,041
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: US 09/019,942
: PRIOR FILING DATE: 1998-02-06
: NUMBER OF SEQ ID NOS: 71
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 50
: LENGTH: 585
: TYPE: DNA
: ORGANISM: Homo sapiens
: IS-09-728-721-50

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Accession	Sequence	Length
Db	CTGACGGATGACGATACCAAGCAGTGGGGGAGGCCAACCAACCAAGATGGG	480
Oy	AAAGCTCTTCAATTTACACACGAGCCTGGAAATCTGACCTTGAAAGATTCCTCTCCAGCC	593
Db	AAGCTCTTCAATTTACACACGAGCCTGGAAATCTGACCTTGAAAGATTCCTCTCCAGCC	540
Oy	CTAAGGAGTCCACGATCCTACCTTGATGAGGACCTGAGCGGAGC	638
Db	CTAAGGAGTCCACGATCCTACCTTGATGAGGACCTGAGCGGAGC	585

Query Match	Similarity	Score	DB	Length
Best Local	Similarity	100.0%	Pred. No. 2.3e-134	Mismatches
Matches	585	Conservative	0	Mismatches
			0	Indels
			0	Gaps
QY	54	ATGGGGCGCGCGCGGAGCCATCCTTGATGCGGTGAGAACTGACCGCCGAGAGCTC	113	
Db	1	ATGGGGCGCGCGCGGAGCCCATCTTGGATGGGTGAGAACTGACCGCCGAGAGCTC	60	
QY	114	AAGAAATTCAAGCTTGAAAGCTGCTGTGGTGCCTGCGCGAGAGGCTACGGGGCATATCCG	173	
Db	61	AAGAAATTCAAGCTTGAAAGCTGCTGTGGTGCCTGCGCGAGAGGCTACGGGGCATATCCG	120	
QY	174	CGGGGGCGGCGTGTCTCCATGAGAGCCCTTTGGACTCACCAGAACACTGTTACGTTTAC	233	
Db	121	CGGGGGCGGCGTGTCTCCATGAGAGCCCTTTGGACTCACCAGAACACTGTTACGTTTAC	180	
QY	234	CTGGAGACCTTAAGGGGCGGAGCTCAACCCCTTAACCTGTGCGGGAATGAGGCTCGAGAG	293	
Db	181	CTGGAGACCTTAAGGGGCGGAGCTCAACCCCTTAACCTGTGCTCGGGAATGAGGCTCGAGAG	240	
QY	294	ATGGCGGGGAGCTGTCAGAGCGGCGCAAGCAAGGGCTCTGGAAGCCGCGCAGACTGGATC	353	
Db	241	ATGGCGGGGAGCTGTCAGAGCGGCGCAAGCAAGGGCTCTGGAAGCCGCGCAGACTGGATC	300	
QY	354	CAGGCCCTCTCTCAATGCGGCGAGCCCAAGCCAGGCTCTGACTTTATAGACAGCAGCGGCT	413	
Db	301	CAGGCCCTCTCTCAATGCGGCGAGCCCAAGCCAGGCTCTGACTTTATAGACAGCAGCGGCT	360	
QY	414	GCGCTTATCGGAGGAGGTCACAAAGCTTAGTGGCTGCGATGCTCTGACGGGAAGTCC	473	
Db	361	GCGCTTATCGGAGGAGGTCACAAAGCTTAGTGGCTGCGATGCTCTGACGGGAAGTCC	420	
QY	474	CTGAAGGATGAGCAATACAGGCAATGGGGGCGAGCCCAACCAACCAAGCAAGATGGCG	533	
Db	421	CTGAAGGATGAGCAATACAGGCAATGGGGGCGAGCCCAACCAACCAAGCAAGATGGCG	480	
QY	534	AAGCTCTTCAAGTTTCACACCAAGCTTGGAACTGAGACTTGCATCAAGACTTGTCTTCCAGGCG	593	


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; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89)...(667)
US-09-728-721-60

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Query Match          45.4%; Score 336; DB 10; Length 777;
Best Local Similarity 72.9%; Pred. No. 2e-73;
Matches 461; Conservative 0; Mismatches 165; Indels 6; Gaps 2;

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QY 18 GGGTGAACGCGGCGACCGCGCGGATCCTGAGCCATGGGCGCGCGCGACGCCATC 77
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DB 53 GAGTAAAGGTGACCGCGCGTGCACCCAGAGCCATGGGCGCGCGAGATGCCATC 112
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QY 78 CTGATGCGCTGGAGACCTGACCGCGCGAGAGTCAAGAGTTCAAGTGAAGTGTGCTG 137
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DB 113 CTGAGAGCTCTTGAAGTCTGATGAGGATGAGACTCAAAAAGTTCAAGATGAAGTGTG 172
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QY 138 TCGGTGCGCGCGGCGACGCGCGATCCCGCGGCGCGCGCTGTCTCATGAGAC 197
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DB 173 ACAGTCACTGCGAGAAAGCTATGGCGCATCCACGCGGCGCGCTGTGAGATGAGAC 232
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QY 198 GCCTTGAGCTCAACCAAGCTGTGACCTTACTGAGACCTAGAGCGCGCGAGCTC 257
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DB 233 GCGATGATCTCACTGACAACTGTGACCTACTATCTGAGTGTGATGCTTGAGCTC 292
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QY 258 ACCGTAAGCTGTGCGCGACATGGCGCTGAGAGATGGCGCGGAGCTGAGAGGCGC 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 293 ACATGACTGTGTTAGACATAGGGCTTACAGAGACTGGCTGAGACGTCGAAAGC--- 349
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QY 318 ACGCACCAGGCTCTGAGAGCGCGCGAGCTGGGATCCAGCGCCCTCTCATGCGGAGCC 377
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DB 350 ACTAAGAGAGAGCTGAGACTGTGGAGCTGAGCAGCAGTGTCCCTCTCAGATACAGCC 409
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QY 378 AAGCCAGGCTGACTTTATAGACCAAGCCAGCGCTGCGTTATCCGAGAGGTACAAAC 437
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DB 410 AGAACAGG---ACACTTTGTGGACACAGCAAGGCAAGCACTCATTTGCCAGGGTACAGAA 466
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QY 438 GTTGAAGTGTGCTGTGATGCTGTACGGGAAGTCTCTGACGATGAGCAGTACAGGCA 497
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QY 498 GTGCGGCGCGAGCCCAACCAAGCAGAGAGTGGAGAGCTCTTCAAGTTTACACAGCC 557
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DB 527 GTTCGTGACAGAGACCAACCAAGATGAGAGAGTCTTCAAGTTTGTTCATCC 586
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QY 558 TGAAGTGAAGCTGCAAGAGCTGTCTCCAGAGCCCTTAAGGAGAGTCCAGTCTCTACTG 617
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DB 587 TGAAGCTGAGCTGCAAGAGCTCTCTCCAGAGCCCTTGAAGAAATACATCTCTACTTG 646
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QY 618 GTGAGAGACTGAGCGAGAGTGAAGGCTCTCT 649
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DB 647 GTGATGAGCTGAGCAGAGCTGAGGTATCTT 678
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RESULT 12
US-09-841-879B-1
; Sequence 1, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

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; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/09/841,879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89)...(667)
US-09-841-879B-1

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Query Match          45.4%; Score 336; DB 10; Length 777;
Best Local Similarity 72.9%; Pred. No. 2e-73;
Matches 461; Conservative 0; Mismatches 165; Indels 6; Gaps 2;

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DB 53 GAGTAAAGGTGACCGCGCGTGCACCCAGAGCCATGGGCGCGCGAGATGCCATC 112
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QY 78 CTGATGCGCTGGAGACCTGACCGCGAGAGTCAAGAGTTCAAGTGAAGTGTGCTG 137
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DB 113 CTGAGAGCTCTTGAAGTCTGATGAGGATGAGACTCAAAAAGTTCAAGATGAAGTGTG 172
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QY 138 TCGGTGCGCGCGGCGACGCGCGATCCCGCGGCGCGCGCTGTCTCATGAGAC 197
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DB 173 ACAGTCACTGCGAGAAAGCTATGGCGCATCCACGCGGCGCGCTGTGAGATGAGAC 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 198 GCCTTGAGCTCAACCAAGCTGTGACCTTACTGAGACCTAGAGCGCGCGAGCTC 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 233 GCGATGATCTCACTGACAACTGTGACCTACTATCTGAGTGTGATGCTTGAGCTC 292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 258 ACCGTAAGCTGTGCGCGACATGGCGCTGAGAGATGGCGCGGAGCTGAGAGGCGC 317
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DB 293 ACATGACTGTGTTAGACATAGGGCTTACAGAGACTGGCTGAGACGTCGAAAGC--- 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 318 ACGCACCAGGCTCTGAGAGCGCGCGAGCTGGGATCCAGCGCCCTCTCATGCGGAGCC 377
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DB 350 ACTAAGAGAGAGCTGAGACTGTGGAGCTGAGCAGCAGTGTCCCTGTGAGATACAGCC 409
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QY 378 AAGCCAGGCTGACTTTATAGACCAAGCCAGCGCTGCGTTATCCGAGAGGTACAAAC 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 410 AGAACAGG---ACACTTTGTGGACACAGCAAGGCAAGCACTCATTTGCCAGGGTACAGAA 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 438 GTTGAAGTGTGCTGTGATGCTGTACGGGAAGTCTCTGACGATGAGCAGTACAGGCA 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 467 GTGAGAGGAGTGTGATGCTTTGCAATGGCAGTGTGCTGACTAGAGACAGTACAGGCA 526
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 498 GTGCGGCGCGAGCCCAACCAAGCAGAGAGTGGAGAGTCTTCAAGTTTACACAGCC 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 527 GTTCGTGACAGAGACCAACCAAGATGAGAGAGTCTTCAAGTTTGTTCATCC 586
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 558 TGAAGTGAAGCTGCAAGAGCTGTCTCCAGAGCCCTTAAGGAGAGTCCAGTCTCTACTG 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 587 TGAAGCTGAGCTGCAAGAGCTCTCTCCAGAGCCCTTGAAGAAATACATCTCTACTTG 646
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 618 GTGAGAGACTGAGCGAGAGTGAAGGCTCTCT 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 647 GTGATGAGCTGAGCAGAGCTGAGGTATCTT 678
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 13
US-09-841-879B-18/c
; Sequence 18, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John

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